SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Koziel, Michael G.
 Desai, Nalini M.
 Lewis, Kelly S.
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 Warren, Gregory W.
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 Crossland, Lyle D.
 Wright, Martha S.
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 Launis, Karen L.
 Rothstein, Steven J.
 Bowman, Cindy G.
 Dawson, John L.
 Dunder, Erik M.
 Pace, Gary M.
 Suttie, Janet L.
- (ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
- (iii) NUMBER OF SEQUENCES: 94
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Syngenta Biotechnology, Inc.
 - (B) STREET: 3054 Cornwallis Road
 - (C) CITY: Research Triangle Park
 - (D) STATE: NC
 - (E) COUNTRY: USA
 - (F) ZIP: 27709
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/547,422
 - (B) FILING DATE: 11-APR-2000
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/459,504
 - (B) FILING DATE: 02-JUN-1995
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/951,715
 - (B) FILING DATE: 25-SEP-1992
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/772,027
 - (B) FILING DATE: 04-OCT-1991

(viii) ATTORNEY/AGENT I	INFORMATION:
-------------------------	--------------

- (A) NAME: Meigs, J. Timothy
- (B) REGISTRATION NUMBER: 38,241
- (C) REFERENCE/DOCKET NUMBER: S-18805I

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (919)541-8587
- (B) TELEFAX: (919)541-8689

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Bacillus thuringiensis kurstaki
 - (B) STRAIN: HD-1
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full-length native

cryIA(b)"

/note= "Appears in Figures 1 and 4 as BTHKURHD."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGATAACA ATCCGAACAT	CAATGAATGC	ATTCCTTATA	ATTGTTTAAG	TAACCCTGAA	60
GTAGAAGTAT TAGGTGGAGA	AAGAATAGAA	ACTGGTTACA	CCCCAATCGA	TATTTCCTTG	120
TCGCTAACGC AATTTCTTTT (GAGTGAATTT	GTTCCCGGTG	CTGGATTTGT	GTTAGGACTA	180
GTTGATATAA TATGGGGAAT	TTTTGGTCCC	TCTCAATGGG	ACGCATTTCT	TGTACAAATT	240
GAACAGTTAA TTAACCAAAG	AATAGAAGAA	TTCGCTAGGA	ACCAAGCCAT	TTCTAGATTA	300
GAAGGACTAA GCAATCTTTA	TCAAATTTAC	GCAGAATCTT	TTAGAGAGTG	GGAAGCAGAT	360
CCTACTAATC CAGCATTAAG	AGAAGAGATG	CGTATTCAAT	TCAATGACAT	GAACAGTGCC	420
CTTACAACCG CTATTCCTCT	TTTTGCAGTT	CAAAATTATC	AAGTTCCTCT	TTTATCAGTA	480
TATGTTCAAG CTGCAAATTT	ACATTTATCA	GTTTTGAGAG	ATGTTTCAGT	GTTTGGACAA	540
AGGTGGGGAT TTGATGCCGC	GACTATCAAT	AGTCGTTATA	ATGATTTAAC	TAGGCTTATT	600
GGCAACTATA CAGATCATGC	TGTACGCTGG	TACAATACGG	GATTAGAGCG	TGTATGGGGA	660
CCGGATTCTA GAGATTGGAT	AAGATATAAT	CAATTTAGAA	GAGAATTAAC	ACTAACTGTA	720
TTAGATATCG TTTCTCTATT	TCCGAACTAT	GATAGTAGAA	CGTATCCAAT	TCGAACAGTT	780

TCCCAATTAA	CAAGAGAAAT	TTATACAAAC	CCAGTATTAG	AAAATTTTGA	TGGTAGTTTT	840
CGAGGCTCGG	CTCAGGGCAT	AGAAGGAAGT	ATTAGGAGTC	CACATTTGAT	GGATATACTT	900
AACAGTATAA	CCATCTATAC	GGATGCTCAT	AGAGGAGAAT	ATTATTGGTC	AGGGCATCAA	960
ATAATGGCTT	CTCCTGTAGG	GTTTTCGGGG	CCAGAATTCA	CTTTTCCGCT	ATATGGAACT	1020
ATGGGAAATG	CAGCTCCACA	ACAACGTATT	GTTGCTCAAC	TAGGTCAGGG	CGTGTATAGA	1080
ACATTATCGT	CCACTTTATA	TAGAAGACCT	TTTAATATAG	GGATAAATAA	TCAACAACTA	1140
TCTGTTCTTG	ACGGGACAGA	ATTTGCTTAT	GGAACCTCCT	CAAATTTGCC	ATCCGCTGTA	1200
TACAGAAAAA	GCGGAACGGT	AGATTCGCTG	GATGAAATAC	CGCCACAGAA	TAACAACGTG	1260
CCACCTAGGC	AAGGATTTAG	TCATCGATTA	AGCCATGTTT	CAATGTTTCG	TTCAGGCTTT	1320
AGTAATAGTA	GTGTAAGTAT	AATAAGAGCT	CCTATGTTCT	CTTGGATACA	TCGTAGTGCT	1380
GAATTTAATA	ATATAATTCC	TTCATCACAA	ATTACACAAA	TACCTTTAAC	AAAATCTACT	1440
AATCTTGGCT	CTGGAACTTC	TGTCGTTAAA	GGACCAGGAT	TTACAGGAGG	AGATATTCTT	1500
CGAAGAACTT	CACCTGGCCA	GATTTCAACC	TTAAGAGTAA	ATATTACTGC	ACCATTATCA	1560
CAAAGATATC	GGGTAAGAAT	TCGCTACGCT	TCTACCACAA	ATTTĄCAATT	CCATACATCA	1620
ATTGACGGAA	GACCTATTAA	TCAGGGGAAT	TTTTCAGCAA	CTATGAGTAG	TGGGAGTAAT	1680
TTACAGTCCG	GAAGCTTTAG	GACTGTAGGT	TTTACTACTC	CGTTTAACTT	TTCAAATGGA	1740
TCAAGTGTAT	TTACGTTAAG	TGCTCATGTC	TTCAATTCAG	GCAATGAAGT	TTATATAGAT	1800
CGAATTGAAT	TTGTTCCGGC	AGAAGTAACC	TTTGAGGCAG	AATATGATTT	AGAAAGAGCA	1860
CAAAAGGCGG	TGAATGAGCT	GTTTACTTCT	TCCAATCAAA	TCGGGTTAAA	AACAGATGTG	1920
ACGGATTATC	ATATTGATCA	AGTATCCAAT	TTAGTTGAGT	GTTTATCTGA	TGAATTTTGT	1980
CTGGATGAAA	AAAAAGAATT	GTCCGAGAAA	GTCAAACATG	CGAAGCGACT	TAGTGATGAG	2040
CGGAATTTAC	TTCAAGATCC	AAACTTTAGA	GGGATCAATA	GACAACTAGA	CCGTGGCTGG	2100
AGAGGAAGTA	CGGATATTAC	CATCCAAGGA	GGCGATGACG	TATTCAAAGA	GAATTACGTT	2160
ACGCTATTGG	GTACCTTTGA	TGAGTGCTAT	CCAACGTATT	TATATCAAAA	AATAGATGAG	2220
TCGAAATTAA	. AAGCCTATAC	CCGTTACCAA	TTAAGAGGGT	ATATCGAAGA	TAGTCAAGAC	2280
TTAGAAATCT	ATTTAATTCG	CTACAATGCC	AAACACGAAA	CAGTAAATGT	GCCAGGTACG	2340
GGTTCCTTAT	GGCCGCTTTC	AGCCCCAAGT	CCAATCGGAA	AATGTGCCCA	TCATTCCCAT	2400
CATTTCTCCT	' TGGACATTGA	TGTTGGATGT	ACAGACTTAA	ATGAGGACTT	AGGTGTATGG	2460
GTGATATTCA	AGATTAAGAC	GCAAGATGGC	CATGCAAGAC	TAGGAAATCT	AGAATTTCTC	2520
GAAGAGAAAC	CATTAGTAGG	AGAAGCACTA	GCTCGTGTGA	AAAGAGCGGA	GAAAAAATGG	2580

AGAGACAAAC	GTGAAAAATT	GGAATGGGAA	ACAAATATTG	TTTATAAAGA	GGCAAAAGAA	2640
TCTGTAGATG	CTTTATTTGT	AAACTCTCAA	TATGATAGAT	TACAAGCGGA	TACCAACATC	2700
GCGATGATTC	ATGCGGCAGA	TAAACGCGTT	CATAGCATTC	GAGAAGCTTA	TCTGCCTGAG	2760
CTGTCTGTGA	TTCCGGGTGT	CAATGCGGCT	ATTTTTGAAG	AATTAGAAGG	GCGTATTTTC	2820
ACTGCATTCT	CCCTATATGA	TGCGAGAAAT	GTCATTAAAA	ATGGTGATTT	TAATAATGGC	2880
TTATCCTGCT	GGAACGTGAA	AGGGCATGTA	GATGTAGAAG	AACAAAACAA	CCACCGTTCG	2940
GTCCTTGTTG	TTCCGGAATG	GGAAGCAGAA	GTGTCACAAG	AAGTTCGTGT	CTGTCCGGGT	3000
CGTGGCTATA	TCCTTCGTGT	CACAGCGTAC	AAGGAGGGAT	ATGGAGAAGG	TTGCGTAACC	3060
ATTCATGAGA	TCGAGAACAA	TACAGACGAA	CTGAAGTTTA	GCAACTGTGT	AGAAGAGGAA	3120
GTATATCCAA	ACAACACGGT	AACGTGTAAT	GATTATACTG	CGACTCAAGA	AGAATATGAG	3180
GGTACGTACA	CTTCTCGTAA	TCGAGGATAT	GACGGAGCCT	ATGAAAGCAA	TTCTTCTGTA	3240
CCAGCTGATT	-ATGCATCAGC	CTATGAAGAA	AAAGCATATA	CAGATGGACG	AAGAGACAAT	3300
CCTTGTGAAT	CTAACAGAGG	ATATGGGGAT	TACACACCAC	TACCAGCTGG	CTATGTGACA	3360
AAAGAATTAG	AGTACTTCCC	AGAAACCGAT	AAGGTATGGA	TTGAGATCGG	AGAAACGGAA	3420
GGAACATTCA	TCGTGGACAG	CGTGGAATTA	CTTCTTATGG	AGGAATAA		3468

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt" /note= "Disclosed in Figure 3 as syn1T.mze"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

60	CAACCCCGAG	ACTGCCTGAG	ATCCCCTACA	CAACGAGTGC	ACCCCAACAT	ATGGACAACA
120	CATCAGCCTG	CCCCCATCGA	ACCGGCTACA	GCGCATCGAG	TGGGCGGCGA	GTGGAGGTGC
180	GCTGGGCCTG	CCGGCTTCGT	GTGCCCGGCG	GAGCGAGTTC	AGTTCCTGCT	AGCCTGACCC
240	GGTGCAGATC	ACGCCTTCCT	AGCCAGTGGG	ርሞሞርርርርርርር	ጥሮሞርርርርር	CTCCACATCA

GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCGCA	ACCAGGCCAT	CAGCCGCCTG	300
GAGGGCCTGA	GCAACCTGTA	CCAGATCTAC	GCCGAGAGCT	TCCGCGAGTG	GGAGGCCGAC	360
CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
CTGACCACCG	CCATCCCCCT	GTTCGCCGTG	CAGAACTACC	AGGTGCCCCT	GCTGAGCGTG	480
TACGTGCAGG	CCGCCAACCT	GCACCTGAGC	GTGCTGCGCG	ACGTGAGCGT	GTTCGGCCAG	540
CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600
GGCAACTACA	CCGACCACGC	CGTGCGCTGG	TACAACACCG	GCCTGGAGCG	CGTGTGGGGC	660
CCCGACAGCC	GCGACTGGAT	CCGCTACAAC	CAGTTCCGCC	GCGAGCTGAC	CCTGACCGTG	720
CTGGACATCG	TGAGCCTGTT	CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
AGCCAGCTGA	CCCGCGAGAT	CTACACCAAC	CCCGTGCTGG	AGAACTTCGA	CGGCAGCTTC	840
CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
AACAGCATCA	- CCATCTACAC	CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA	GCCCCGTGGG	CTTCAGCGGC	CCCGAGTTCA	CCTTCCCCCT	GTACGGCACC	1020
ATGGGCAACG	CCGCCCCCA	GCAGCGCATC	GTGGCCCAGC	TGGGCCAGGG	CGTGTACCGC	1080
ACCCTGAGCA	GCACCCTGTA	CCGCCGCCCC	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
AGCGTGCTGG	ACGGCACCGA	GTTCGCCTAC	GGCACCAGCA	GCAACCTGCC	CAGCGCCGTG	1200
TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCCAGAA	CAACAACGTG	1260
CCCCCCCGCC	AGGGCTTCAG	CCACCGCCTG	AGCCACGTGA	GCATGTTCCG	CAGCGGCTTC	1320
AGCAACAGCA	GCGTGAGCAT	CATCCGCGCC	CCCATGTTCA	GCTGGATCCA	CCGCAGCGCC	1380
GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC	GCGTGCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT	TCGTGCCCGC	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGCGCGCC	1860
CAGAAGGCCG	TGAACGAGCT	GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC	ACATCGACCA	GGTGAGCAAC	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040

ርርር a a ርርጥርር	ጥርቦልርርልሮር	CAACTTCCGC	GGCATCAACC	GCCAGCTGGA	CCGCGGCTGG	2103
						2163
			GGCGACGACG			
ACCCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2223
AGCAAGCTGA	AGGCCTACAC	CCGCTACCAG	CTGCGCGGCT	ACATCGAGGA	CAGCCAGGAC	2283
CTGGAGATCT	ACCTGATCCG	CTACAACGCC	AAGCACGAGA	CCGTGAACGT	GCCCGGCACC	2340
GGCAGCCTGT	GGCCCCTGAG	CGCCCCAGC	CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
CACTTCAGCC	TGGACATCGA	CGTGGGCTGC	ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460
GTGATCTTCA	AGATCAAGAC	CCAGGACGGC	CACGCCCGCC	TGGGCAACCT	GGAGTTCCTG	2520
GAGGAGAAGC	CCCTGGTGGG	CGAGGCCCTG	GCCCGCGTGA	AGCGCGCCGA	GAAGAAGTGG	2580
CGCGACAAGC	GCGAGAAGCT	GGAGTGGGAG	ACCAACATCG	TGTACAAGGA	GGCCAAGGAG	2640
AGCGTGGACG	CCCTGTTCGT	GAACAGCCAG	TACGACCGCC	TGCAGGCCGA	CACCAACATC	2700
GCCATGATCC	ACGCCGCCGA	CAAGCGCGTG	CACAGCATCC	GCGAGGCCTA	CCTGCCCGAG	2760
CTGAGCGTGA	TCCCCGGCGT	GAACGCCGCC	ATCTTCGAGG	AGCTGGAGGG	CCGCATCTTC	2820
ACCGCCTTCA	GCCTGTACGA	CGCCCGCAAC	GTGATCAAGA	ACGGCGACTT	CAACAACGGC	2880
CTGAGCTGCT	GGAACGTGAA	GGGCCACGTG	GACGTGGAGG	AGCAGAACAA	CCACCGCAGC	2940
GTGCTGGTGG	TGCCCGAGTG	GGAGGCCGAG	GTGAGCCAGG	AGGTGCGCGT	GTGCCCCGGC	3000
CGCGGCTACA	TCCTGCGCGT	GACCGCCTAC	AAGGAGGGCT	ACGGCGAGGG	CTGCGTGACC	3060
ATCCACGAGA	TCGAGAACAA	CACCGACGAG	CTGAAGTTCA	GCAACTGCGT	GGAGGAGGAG	3120
GTGTACCCCA	ACAACACCGT	GACCTGCAAC	GACTACACCG	CCACCCAGGA	GGAGTACGAG	3180
GGCACCTACA	CCAGCCGCAA	CCGCGGCTAC	GACGGCGCCT	ACGAGAGCAA	CAGCAGCGTG	3240
CCCGCCGACT	ACGCCAGCGC	CTACGAGGAG	AAGGCCTACA	CCGACGGCCG	CCGCGACAAC	3300
CCCTGCGAGA	GCAACCGCGG	CTACGGCGAC	TACACCCCCC	TGCCCGCCGG	CTACGTGACC	3360
AAGGAGCTGG	AGTACTTCCC	CGAGACCGAC	AAGGTGTGGA	TCGAGATCGG	CGAGACCGAG	3420
GGCACCTTCA	TCGTGGACAG	CGTGGAGCTG	CTGCTGATGG	AGGAGTAG		3468

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1947 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1947
- (D) OTHER INFORMATION: /product= "Truncated synthetic maize optimized cryIA(b) gene" /note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

			~			(,
60	CAACCCCGAG	ACTGCCTGAG	ATCCCCTACA	CAACGAGTGC	ACCCCAACAT	ATGGACAACA
120	CATCAGCCTG	CCCCCATCGA	ACCGGCTACA	GCGCATCGAG	TGGGCGGCGA	GTGGAGGTGC
180	GCTGGGCCTG	CCGGCTTCGT	GTGCCCGGCG	GAGCGAGTTC	AGTTCCTGCT	AGCCTGACCC
240	GGTGCAGATC	ACGCCTTCCT	AGCCAGTGGG	CTTCGGCCCC	TCTGGGGCAT	GTGGACATCA
300	CAGCCGCCTG	ACCAGGCCAT	TTCGCCCGCA	CATCGAGGAG	TCAACCAGCG	GAGCAGCTGA
360	GGAGGCCGAC	TCCGCGAGTG	GCCGAGAGCT	CCAAATCTAC	GCAACCTGTA	GAGGGCCTGA
420	GAACAGCGCC	TCAACGACAT	CGCATCCAGT	CGAGGAGATG	CCGCCCTGCG	CCCACCAACC
480	GCTGAGCGTG	AGGTGCCCCT	CAGAACTACC	GTTCGCCGTG	CCATCCCCCT	CTGACCACCG
540	GTTCGGCCAG	ACGTÇAGCGT	GTGCTGCGCG	GCACCTGAGC	CCGCCAACCT	TACGTGCAGG
600	CCGCCTGATC	ACGACCTGAC	AGCCGCTACA	CACCATCAAC	TCGACGCCGC	CGCTGGGGCT
660	CGTGTGGGGT	GCCTGGAGCG	TACAACACCG	CGTGCGCTGG	CCGACCACGC	GGCAACTACA
720	CCTGACCGTG	GCGAGCTGAC	CAGTTCCGCC	CAGGTACAAC	GCGACTGGAT	CCCGACAGCC
780	CCGCACCGTG	CCTACCCCAT	GACAGCCGCA	CCCCAACTAC	TGAGCCTGTT	CTGGACATCG
840	CGGCAGCTTC	AGAACTTCGA	CCCGTGCTGG	TTACACCAAC	CCCGCGAGAT	AGCCAGCTGA
900	GGACATCCTG	CCCACCTGAT	ATCCGCAGCC	CGAGGGCAGC	CCCAGGGCAT	CGCGGCAGCG
960	CGGCCACCAG	ACTACTGGAG	CGCGGCGAGT	CGACGCCCAC	CCATCTACAC	AACAGCATCA
1020	GTACGGCACC	CCTTCCCCCT	CCCGAGTTCA	CTTCAGCGGC	GCCCCGTCGG	ATCATGGCCA
1080	AGTGTACCGC	TGGGCCAGGG	GTGGCACAGC	GCAGCGCATC	CTGCACCTCA	ATGGGCAACG
1140	CCAGCAGCTG	GCATCAACAA	TTCAACATCG	CCGTCGACCT	GCACCCTGTA	ACCCTGAGCA
1200	CAGCGCCGTG	GCAACCTGCC	GGCACCAGCA	GTTCGCCTAC	ACGGCACCGA	AGCGTGCTGG
1260	CAACAACGTG	CCCCTCAGAA	GACGAGATCC	GGACAGCCTG	GCGGCACCGT	TACCGCAAGA
1320	CAGTGGCTTC	GCATGTTCCG	AGCCACGTGA	CCACCGTCTG	AGGGCTTCAG	CCACCTCGAC
1380	CCGCAGTGCC	GCTGGATTCA	CCTATGTTCA	CATCCGTGCA	GCGTGAGCAT	AGCAACAGCA
1440	CAAGAGCACC	TCCCCCTGAC	ATCACCCAGA	CAGCAGCCAA	ACATCATCCC	GAGTTCAACA
1500	CGACATCCTG	TCACCGGCGG	GGCCCCGGCT	CGTGGTGAAG	GCGGCACCAG	AACCTGGGCA

CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC	GCGTCCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT	TCGTGCCCGC	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGAGGGCT	1860
CAGAAGGCCG	TGAACGAGCT	GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC	ACATCGATCA	GGTGTAG				1947

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized" /note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

60	CAACCCCGAG	ACTGCCTGAG	ATCCCCTACA	CAACGAGTGC	ACCCCAACAT	ATGGACAACA
120	CATCAGCCTG	CCCCCATCGA	ACCGGCTACA	GCGCATCGAG	TGGGCGGCGA	GTGGAGGTGC
180	GCTGGGCCTG	CCGGCTTCGT	GTGCCCGGCG	GAGCGAGTTC	AGTTCCTGCT	AGCCTGACCC
240	GGTGCAGATC	ACGCCTTCCT	AGCCAGTGGG	CTTCGGCCCC	TCTGGGGCAT	GTGGACATCA
300	CAGCCGCCTG	ACCAGGCCAT	TTCGCCCGCA	CATCGAGGAG	TCAACCAGCG	GAGCAGCTGA
360	GGAGGCCGAC	TCCGCGAGTG	GCCGAGAGCT	CCAAATCTAC	GCAACCTGTA	GAGGGCCTGA
420	GAACAGCGCC	TCAACGACAT	CGCATCCAGT	CGAGGAGATG	CCGCCCTGCG	CCCACCAACC
480	GCTGAGCGTG	AGGTGCCCCT	CAGAACTACC	GTTCGCCGTG	CCATCCCCCT	CTGACCACCG
540	GTTCGGCCAG	ACGTCAGCGT	GTGCTGCGCG	GCACCTGAGC	CCGCCAACCT	TACGTGCAGG
600	CCGCCTGATC	ACGACCTGAC	AGCCGCTACA	CACCATCAAC	TCGACGCCGC	CGCTGGGGCT

GGCAACTACA CCGACCAC	GC CGTGCGCTGG	TACAACACCG	GCCTGGAGCG	CGTGTGGGGT	660
CCCGACAGCC GCGACTGG	AT CAGGTACAAC	CAGTTCCGCC	GCGAGCTGAC	CCTGACCGTG	720
CTGGACATCG TGAGCCTG	TT CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
AGCCAGCTGA CCCGCGAG	AT TTACACCAAC	CCCGTGCTGG	AGAACTTCGA	CGGCAGCTTC	840
CGCGGCAGCG CCCAGGGC	AT CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
AACAGCATCA CCATCTAC	AC CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA GCCCCGTC	GG CTTCAGCGGC	CCCGAGTTCA	CCTTCCCCCT	GTACGGCACC	1020
ATGGGCAACG CTGCACCT	CA GCAGCGCATC	GTGGCACAGC	TGGGCCAGGG	AGTGTACCGC	1080
ACCCTGAGCA GCACCCTG	TA CCGTCGACCT	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
AGCGTGCTGG ACGGCACC	GA GTTCGCCTAC	GGCACCAGCA	GCAACCTGCC	CAGCGCCGTG	1200
TACCGCAAGA GCGGCACC	GT GGACAGCCTG	GACGAGATCC	CCCCTCAGAA	CAACAACGTG	1260
CCACCTCGAC AGGGCTTC	AG CCACCGTCTG	AGCCACGTGA	GCATGTTCCG	CAGTGGCTTC	1320
AGCAACAGCA GCGTGAGC	AT CATCCGTGCA	CCTATGTTCA	GCTGGATTCA	CCGCAGTGCC	1380
GAGTTCAACA ACATCATC	CC CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA GCGGCACC	AG CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
CGCCGCACCA GCCCCGGC	CA GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC GCGTCCGC	CAT CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGCC GCCCCATC	CAA CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG GCAGCTTC	CCG CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT TCACCCTC	GAG CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT TCGTGCCC	CGC CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGAGGGCT	1860
CAGAAGGCCG TGAACGAG	GCT GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC ACATCGAT	rca ggtgagcaac	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA AGAAGGAG	GCT GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040
CGCAACCTGC TGCAGGAG	CCC CAACTTCCGC	GGCATCAACC	GCCAGCTGGA	CCGCGGCTGG	2100
CGCGGCAGCA CCGACATO	CAC CATCCAGGGC	GGCGACGACG	TGTTCAAGGA	GAACTACGTG	2160
ACCCTGCTGG GCACCTT	CGA CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
AGCAAGCTGA AGGCCTAG	CAC CCGCTACCAC	CTGCGCGGCT	ACATCGAGGA	CAGCCAGGAC	2280
CTGGAGATCT ACCTGATO	CCG CTACAACGCC	: AAGCACGAGA	CCGTGAACGT	GCCCGGCACC	2340
GGCAGCCTGT GGCCCCTG	GAG CGCCCCAGC	: CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
CACTTCAGCC TGGACAT	CGA CGTGGGCTGC	: ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460

GTGATCTTCA	AGATCAAGAC	CCAGGACGGC	CACGCCCGCC	TGGGCAACCT	GGAGTTCCTG	2520
GAGGAGAAGC	CCCTGGTGGG	CGAGGCCCTG	GCCCGCGTGA	AGCGCGCCGA	GAAGAAGTGG	2580
CGCGACAAGC	GCGAGAAGCT	GGAGTGGGAG	ACCAACATCG	TGTACAAGGA	GGCCAAGGAG	2640
AGCGTGGACG	CCCTGTTCGT	GAACAGCCAG	TACGACCGCC	TGCAGGCCGA	CACCAACATC	2700
GCCATGATCC	ACGCCGCCGA	CAAGCGCGTG	CACAGCATTC	GCGAGGCCTA	CCTGCCCGAG	2760
CTGAGCGTGA	TCCCCGGCGT	GAACGCCGCC	ATCTTCGAGG	AGCTGGAGGG	CCGCATCTTC	2820
ACCGCCTTCA	GCCTGTACGA	CGCCCGCAAC	GTGATCAAGA	ACGGCGACTT	CAACAACGGC	2880
CTGAGCTGCT	GGAACGTGAA	GGGCCACGTG	GACGTGGAGG	AGCAGAACAA	CCACCGCAGC	2940
GTGCTGGTGG	TGCCCGAGTG	GGAGGCCGAG	GTGAGCCAGG	AGGTGCGCGT	GTGCCCCGGC	3000
CGCGGCTACA	TCCTGCGCGT	GACCGCCTAC	AAGGAGGGCT	ACGGCGAGGG	CTGCGTGACC	3060
ATCCACGAGA	TCGAGAACAA	CACCGACGAG	CTCAAGTTCA	GCAACTGCGT	GGAGGAGGAG	3120
GTGTACCCCA	ACAACACCGT	GACCTGCAAC	GACTACACCG	CCACCCAGGA	GGAGTACGAG	3180
GGCACCTACA	CCAGCCGCAA	CCGCGGCTAC	GACGGCGCCT	ACGAGAGCAA	CAGCAGCGTG	3240
CCCGCCGACT	ACGCCAGCGC	CTACGAGGAG	AAGGCCTACA	CCGACGGCCG	CCGCGACAAC	3300
CCCTGCGAGA	GCAACCGCGG	CTACGGCGAC	TACACCCCCC	TGCCCGCCGG	CTACGTGACC	3360
AAGGAGCTGG	AGTACTTCCC	CGAGACCGAC	AAGGTGTGGA	TCGAGATCGG	CGAGACCGAG	3420
GGCACCTTCA	TCGTGGACAG	CGTGGAGCTG	CTGCTGATGG	AGGAGTAG		3468

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1845 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..1845
 - (D) OTHER INFORMATION: /note= "This is the synthetic Bt gene according to Perlak et al. as shown in Figures 4 and 5 as PMONBT."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACAACA ACCCAAACAT CAACGAATGC ATTCCATACA ACTGCTTGAG TAACCCAGAA

GTTGAAGTAC TTGGTGGAGA ACGCATTGAA ACCGGTTACA CTCCCATCGA CATCTCCTTG 120 TCCTTGACAC AGTTTCTGCT CAGCGAGTTC GTGCCAGGTG CTGGGTTCGT TCTCGGACTA 180 GTTGACATCA TCTGGGGTAT CTTTGGTCCA TCTCAATGGG ATGCATTCCT GGTGCAAATT 240 GAGCAGTTGA TCAACCAGAG GATCGAAGAG TTCGCCAGGA ACCAGGCCAT CTCTAGGTTG 300 GAAGGATTGA GCAATCTCTA CCAAATCTAT GCAGAGAGCT TCAGAGAGTG GGAAGCCGAT 360 CCTACTAACC CAGCTCTCCG CGAGGAAATG CGTATTCAAT TCAACGACAT GAACAGCGCC 420 TTGACCACAG CTATCCCATT GTTCGCAGTC CAGAACTACC AAGTTCCTCT CTTGTCCGTG 480 TACGTTCAAG CAGCTAATCT TCACCTCAGC GTGCTTCGAG ACGTTAGCGT GTTTGGGCAA 540 AGGTGGGGAT TCGATGCTGC AACCATCAAT AGCCGTTACA ACGACCTTAC TAGGCTGATT 600 GGAAACTACA CCGACCACGC TGTTCGTTGG TACAACACTG GCTTGGAGCG TGTCTGGGGT 660 720 CCTGATTCTA GAGATTGGAT TAGATACAAC CAGTTCAGGA GAGAATTGAC CCTCACAGTT TTGGACATTG TGTCTCTTT CCCGAACTAT GACTCCAGAA CCTACCCTAT CCGTACAGTG 780 TCCCAACTTA CCAGAGAAAT CTATACTAAC CCAGTTCTTG AGAACTTCGA CGGTAGCTTC 840 CGTGGTTCTG CCCAAGGTAT CGAAGGCTCC ATCAGGAGCC CACACTTGAT GGACATCTTG 900 AACAGCATAA CTATCTACAG CGATGCTCAC AGAGGAGAGT ATTACTGGTC TGGACACCAG 960 ATCATGGCCT CTCCAGTTGG ATTCAGCGGG CCCGAGTTTA CCTTTCCTCT CTATGGAACT 1020 ATGGGAAACG CCGCTCCACA ACAACGTATC GTTGCTCAAC TAGGTCAGGG TGTCTACAGA 1080 ACCTTGTCTT CCACCTTGTA CAGAAGACCC TTCAATATCG GTATCAACAA CCAGCAACTT 1140 TCCGTTCTTG ACGGAACAGA GTTCGCCTAT GGAACCTCTT CTAACTTGCC ATCCGCTGTT 1200 TACAGAAAGA GCGGAACCGT TGATTCCTTG GACGAAATCC CACCACAGAA CAACAATGTG 1260 CCACCCAGGC AAGGATTCTC CCACAGGTTG AGCCACGTGT CCATGTTCCG TTCCGGATTC 1320 AGCAACAGTT CCGTGAGCAT CATCAGAGCT CCTATGTTCT CATGGATTCA TCGTAGTGCT 1380 GAGTTCAACA ATATCATTCC TTCCTCTCAA ATCACCCAAA TCCCATTGAC CAAGTCTACT 1440 AACCTTGGAT CTGGAACTTC TGTCGTGAAA GGACCAGGCT TCACAGGAGG TGATATTCTT 1500 AGAAGAACTT CTCCTGGCCA GATTAGCACC CTCAGAGTTA ACATCACTGC ACCACTTTCT 1560 CAAAGATATC GTGTCAGGAT TCGTTACGCA TCTACCACTA ACTTGCAATT CCACACCTCC 1620 ATCGACGGAA GGCCTATCAA TCAGGGTAAC TTCTCCGCAA CCATGTCAAG CGGCAGCAAC 1680 TTGCAATCCG GCAGCTTCAG AACCGTCGGT TTCACTACTC CTTTCAACTT CTCTAACGGA 1740 TCAAGCGTTT TCACCCTTAG CGCTCATGTG TTCAATTCTG GCAATGAAGT GTACATTGAC 1800 1845 CGTATTGAGT TTGTGCCTGC CGAAGTTACC TTCGAGGCTG AGTAC

(2) INFORMATION FOR SEQ ID NO:6:

1	' i	CECTENCE	CHARACTERISTICS:
١	ι Τ) PEGOENCE	CHARACIERISTICS

- (A) LENGTH: 3624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3621
- (D) OTHER INFORMATION: /product= "Full-length, maize
 optmized cryIB"
 /note= "Disclosed in Figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG Met 1	GAC Asp	CTG Leu	CTG Leu	CCC Pro 5	GAC Asp	GCC Ala	CGC Arg	ATC Ile	GAG Glu 10	GAC Asp	AGC Ser	CTG Leu	TGC Cys	ATC Ile 15	GCC Ala	4	48
GAG Glu	GGC Gly	AAC Asn	AAC Asn 20	ATC Ile	GAC Asp	CCC Pro	TTC Phe	GTG Val 25	AGC Ser	GCC Ala	AGC Ser	ACC Thr	GTG Val 30	CAG Gln	ACC Thr	9	96
GGC Gly	ATC Ile	AAC Asn 35	ATC Ile	GCC Ala	GGC Gly	CGC Arg	ATC Ile 40	CTG Leu	GGC Gly	GTG Val	CTG Leu	GGC Gly 45	GTG Val	CCC Pro	TTC Phe	14	44
GCC Ala	GGC Gly 50	CAG Gln	CTG Leu	GCC Ala	AGC Ser	TTC Phe 55	TAC Tyr	AGC Ser	TTC Phe	CTG Leu	GTG Val 60	GGC Gly	GAG Glu	CTG Leu	TGG Trp	19	92
CCC Pro 65	CGC Arg	GGC Gly	CGC Arg	GAC Asp	CAG Gln 70	TGG Trp	GAG Glu	ATC Ile	TTC Phe	CTG Leu 75	GAG Glu	CAC His	GTG Val	GAG Glu	CAG Gln 80	2	40
CTG Leu	ATC Ile	AAC Asn	CAG Gln	CAG Gln 85	ATC Ile	ACC Thr	GAG Glu	AAC Asn	GCC Ala 90	CGC Arg	AAC Asn	ACC Thr	GCC Ala	CTG Leu 95	GCC Ala	2	88
CGC Arg	CTG Leu	CAG Gln	GGC Gly 100	CTG Leu	GGC Gly	GAC Asp	AGC Ser	TTC Phe 105	CGC Arg	GCC Ala	TAC Tyr	CAG Gln	CAG Gln 110	AGC Ser	CTG Leu	3:	36
GAG Glu	GAC Asp	TGG Trp 115	CTG Leu	GAG Glu	AAC Asn	CGC Arg	GAC Asp 120	GAC Asp	GCC Ala	CGC Arg	ACC Thr	CGC Arg 125	AGC Ser	GTG Val	CTG Leu	3	84
TAC Tyr	ACC Thr 130	CAG Gln	TAC Tyr	ATC Ile	GCC Ala	CTG Leu 135	GAG Glu	CTG Leu	GAC Asp	TTC Phe	CTG Leu 140	AAC Asn	GCC Ala	ATG Met	CCC Pro	4	32
CTG Leu	TTC Phe	GCC Ala	ATC Ile	CGC Arg	AAC Asn	CAG Gln	GAG Glu	GTG Val	CCC Pro	CTG Leu	CTG Leu	ATG Met	GTG Val	TAC Tyr	GCC Ala	4	80

145					150					155					160	
CAG Gln	GCC Ala	GCC Ala	AAC Asn	CTG Leu 165	CAC His	CTG Leu	CTG Leu	CTG Leu	CTG Leu 170	CGC Arg	GAC Asp	GCC Ala	AGC Ser	CTG Leu 175	TTC Phe	528
GGC Gly	AGC Ser	GAG Glu	TTC Phe 180	GGC Gly	CTG Leu	ACC Thr	AGC Ser	CAG Gln 185	GAG Glu	ATC Ile	CAG Gln	CGC Arg	TAC Tyr 190	TAC Tyr	GAG Glu	576
CGC Arg	CAG Gln	GTG Val 195	GAG Glu	CGC Arg	ACC Thr	CGC Arg	GAC Asp 200	TAC Tyr	AGC Ser	GAC Asp	TAC Tyr	TGC Cys 205	GTG Val	GAG Glu	TGG Trp	624
TAC Tyr	AAC Asn 210	ACC Thr	GGC Gly	CTG Leu	AAC Asn	AGC Ser 215	CTG Leu	CGC Arg	GGC Gly	ACC Thr	AAC Asn 220	GCC Ala	GCC Ala	AGC Ser	TGG Trp	672
GTG Val 225	CGC Arg	TAC Tyr	AAC Asn	CAG Gln	TTC Phe 230	CGC Arg	CGC Arg	GAC Asp	CTG Leu	ACC Thr 235	CTG Leu	GGC Gly	GTG Val	CTG Leu	GAC Asp 240	720
CTG Leu	GTG Val	GCC- Ala	CTG Leu	TTC Phe 245	CCC Pro	AGC Ser	TAC Tyr	GAC Asp	ACC Thr 250	CGC Arg	ACC Thr	TAC Tyr	CCC Pro	ATC Ile 255	AAC Asn	768
ACC Thr	AGC Ser	GCC Ala	CAG Gln 260	CTG Leu	ACC Thr	CGC Arg	GAG Glu	GTG Val 265	TAC Tyr	ACC Thr	GAC Asp	GCC Ala	ATC Ile 270	GGC Gly	GCC Ala	816
ACC Thr	GGC Gly	GTG Val 275	AAC Asn	ATG Met	GCC Ala	AGC Ser	ATG Met 280	AAC Asn	TGG Trp	TAC Tyr	AAC Asn	AAC Asn 285	AAC Asn	GCC Ala	CCC Pro	864
AGC Ser	TTC Phe 290	AGC Ser	GCC Ala	ATC Ile	GAG Glu	GCC Ala 295	GCC Ala	GCC Ala	ATC Ile	CGC Arg	AGC Ser 300	CCC Pro	CAC His	CTG Leu	CTG Leu	912
GAC Asp 305	TTC Phe	CTG Leu	GAG Glu	CAG Gln	CTG Leu 310	ACC Thr	ATC Ile	TTC Phe	AGC Ser	GCC Ala 315	AGC Ser	AGC Ser	CGC Arg	TGG Trp	AGC Ser 320	960
AAC Asn	ACC Thr	CGC Arg	CAC His	ATG Met 325	ACC Thr	TAC Tyr	TGG Trp	CGC Arg	GGC Gly 330	His	ACC Thr	ATC Ile	CAG Gln	AGC Ser 335	CGC Arg	1008
CCC Pro	ATC Ile	GGC Gly	GGC Gly 340	Gly	CTG Leu	AAC Asn	ACC Thr	AGC Ser 345	ACC Thr	CAC His	GGC Gly	GCC Ala	ACC Thr 350	AAC Asn	ACC Thr	1056
AGC Ser	ATC Ile	AAC Asn 355	Pro	GTG Val	ACC Thr	CTG Leu	CGC Arg 360	Phe	GCC Ala	AGC Ser	CGC Arg	GAC Asp 365	GTG Val	TAC Tyr	CGC Arg	1104
ACC Thr	GAG Glu 370	AGC Ser	TAC Tyr	GCC Ala	GGC Gly	GTG Val 375	Leu	CTG Leu	TGG Trp	GGC Gly	ATC Ile 380	Tyr	CTG Leu	GAG Glu	CCC Pro	1152
ATC Ile 385	CAC His	GGC Gly	GTG Val	CCC	ACC Thr 390	Val	CGC Arg	TTC Phe	AAC Asn	TTC Phe 395	Thr	AAC Asn	CCC Pro	CAG Gln	AAC Asn 400	1200

ATC Ile	AGC Ser	GAC Asp	CGC Arg	GGC Gly 405	ACC Thr	GCC Ala	AAC Asn	TAC Tyr	AGC Ser 410	CAG Gln	CCC Pro	TAC Tyr	GAG Glu	AGC Ser 415	CCC Pro	1248
GGC	CTG Leu	CAG Gln	CTG Leu 420	AAG Lys	GAC Asp	AGC Ser	GAG Glu	ACC Thr 425	GAG Glu	CTG Leu	CCC Pro	CCC Pro	GAG Glu 430	ACC Thr	ACC Thr	129€
GAG Glu	CGC Arg	CCC Pro 435	AAC Asn	TAC Tyr	GAG Glu	AGC Ser	TAC Tyr 440	AGC Ser	CAC His	CGC Arg	CTG Leu	AGC Ser 445	CAC His	ATC Ile	GGC Gly	1344
ATC Ile	ATC Ile 450	CTG Leu	CAG Gln	AGC Ser	CGC Arg	GTG Val 455	AAC Asn	GTG Val	CCC Pro	GTG Val	TAC Tyr 460	AGC Ser	TGG Trp	ACC Thr	CAC His	1392
CGC Arg 465	AGC Ser	GCC Ala	GAC Asp	CGC Arg	ACC Thr 470	AAC Asn	ACC Thr	ATC Ile	GGC Gly	CCC Pro 475	AAC Asn	CGC Arg	ATC Ile	ACC Thr	CAG Gln 480	1445
ATC Ile	CCC Pro	ATG Met	GTG Val	AAG Lys 485	GCC Ala	AGC Ser	GAG Glu	CTG Leu	CCC Pro 490	CAG Gln	GGC Gly	ACC Thr	ACC Thr	GTG Val 495	GTG Val	1483
CGC Arg	GGC Gly	CCC Pro	GGC Gly 500	TTC Phe	ACC Thr	GGC Gly	GGC Gly	GAC Asp 505	ATC Ile	CTG Leu	CGC Arg	CGC Arg	ACC Thr 510	Asn	ACC Thr	1536
GGC Gly	GGC Gly	TTC Phe 515	GGC Gly	CCC Pro	ATC Ile	CGC Arg	GTG Val 520	ACC Thr	GTG Val	AAC Asn	GGC Gly	CCC Pro 525	CTG Leu	ACC Thr	CAG Gln	158 <u>4</u>
CGC Arg	TAC Tyr 530	CGC Arg	ATC Ile	GGC Gly	TTC Phe	CGC Arg 535	TAC Tyr	GCC Ala	AGC Ser	ACC Thr	GTG Val 540	GAC Asp	TTC Phe	GAC Asp	TTC Phe	1632
TTC Phe 545	GTG Val	AGC Ser	CGC Arg	GGC Gly	GGC Gly 550	ACC Thr	ACC Thr	GTG Val	AAC Asn	AAC Asn 555	TTC Phe	CGC Arg	TTC Phe	CTG Leu	CGC Arg 560	1680
ACC Thr	ATG Met	AAC Asn	AGC Ser	GGC Gly 565	Asp	GAG Glu	CTG Leu	AAG Lys	TAC Tyr 570	GGC Gly	AAC Asn	TTC Phe	GTG Val	CGC Arg 575	CGC Arg	1728
GCC Ala	TTC Phe	ACC Thr	ACC Thr 580	Pro	TTC Phe	ACC Thr	TTC Phe	ACC Thr 585	CAG Gln	ATC Ile	CAG Gln	GAC Asp	ATC Ile 590	ATC Ile	CGC Arg	1776
ACC Thr	AGC Ser	ATC Ile 595	Gln	GGC Gly	CTG Leu	AGC Ser	GGC Gly 600	Asn	GGC	GAG Glu	GTG Val	TAC Tyr 605	ATC Ile	GAC Asp	AAG Lys	1824
ATC Ile	GAG Glu 610	Ile	ATC Ile	CCC	GTG Val	ACC Thr 615	Ala	ACC Thr	TTC Phe	GAG Glu	GCC Ala 620	GAG Glu	TAC Tyr	GAC Asp	CTG Leu	1872
GAG Glu 625	CGC Arg	GCC Ala	CAG Gln	GAG Glu	GCC Ala 630	Val	AAC Asn	GCC Ala	CTG Leu	TTC Phe 635	Thr	AAC Asn	ACC Thr	AAC Asn	CCC Pro 640	1920

					GAC Asp											1963
					CTG Leu											2016
					GTG Val											2064
					CCC Pro											2112
					GAG Glu 710											2163
					TGG Trp											2208
					GAG Glu											2256
					TAC Tyr									GAG		230≟
					TAC Tyr											2352
					CTG Leu 790											2400
					GAG Glu											2448
					GAG Glu											2496
					TGC Cys											2544
					AGC Ser											2592
					GTG Val 870											2640
GGC	CAC	GCC	CGC	CTG	GGC	AAC	CTG	GAG	TTC	ATC	GAG	GAG	AAG	CCC	CTG	2688

Gly	His	Ala	Arg	Leu 885	Gly	Asn	Leu	Glu	Phe 890	Ile	Glu	Glu	Lys	Pro 895	Leu	
															CGC Arg	2736
															GAG Glu	2784
		GAG Glu														2832
		GCC Ala													CTG Leu 960	2880
		CGC Arg														2928
		AAC Asn														2976
		AGC Ser 995						Asn					Gly			3024
		GGC Gly)					Asn					Val				3072
	Ser	CAC His				Asp					Glu					3120
		CAG Gln	Ala		Arg	Val	Cys	Pro	Gly	Cys		Tyr		Leu	Arg	3168
		GCC Ala		Lys					Glu					Ile	CAC His	3216
GAG				•					•				10/0			
		GAG Glu 1075	AAC Asn	AAC			_	CTG Leu	AAG	-			CGC Arg	GAG		3264
Glu GAG	Ile GAG	Glu 1075 GTG Val	AAC Asn TAC	AAC Asn	Thr	Asp	Glu 1080 ACC Thr	CTG Leu GGC	AAG Lys ACC	Phe TGC	Lys AAC	Asn 1085 GAC Asp	CGC Arg	GAG Glu ACC	Glu GCC	3264 3312
Glu GAG Glu CAC	GAG Glu 1090 CAG Gln	Glu 1075 GTG Val	AAC Asn TAC Tyr	AAC Asn CCC Pro	Thr ACC Thr	GAC Asp 1095 TGC Cys	Glu 1080 ACC Thr	CTG Leu GGC Gly	AAG Lys ACC Thr	Phe TGC Cys	AAC ASN 1100 AAC ASN	Asn 1085 GAC Asp	CGC Arg TAC Tyr	GAG Glu ACC Thr	GCC GCC Ala	

				Glu					Thr					Asp	AAC Asn	3456
			Tyr					Val					Val		GCC Ala	3504
GGC Gly	TAC Tyr 117	Val	ACC Thr	AAG Lys	GAG Glu	CTG Leu 117	Glu	TAC Tyr	TTC Phe	CCC Pro	GAG Glu 118	Thr	GAC Asp	ACC Thr	GTG Val	3552
	Ile					Thr					Ile				GTG Val 1200	3600
				ATG Met 120	Glu		TAG									3624
(2)	INF	ORMAC	FION	FOR	SEQ	ID N	10:7:	:								
		(i) §	(A)	ENCE) LEI) TYI) TOI	NGTH	: 120 amino)7 ar o aci	nino Id		ds		,		٠.		
	(:	ii) N	OLE	CULE	TYPE	E: pı	rotei	n								
	(2	ki) S	SEQUI	ENCE	DESC	CRIPI	CION:	SEQ	Q ID	NO:	7:					
Met 1	Asp	Leu	Leu	Pro 5	Asp	Ala	Arg	Ile	Glu 10	Asp	Ser	Leu	Cys	Ile 15	Ala	
Glu	Gly	Asn	Asn 20	Ile	Asp	Pro	Phe	Val 25	Ser	Ala	Ser	Thr	Val 30	Gln	Thr	
Gly	Ile	Asn 35	Ile	Ala	Gly	Arg	Ile 40	Leu	Gly	Val	Leu	Gly 45	Val	Pro	Phe	
Ala	Gly 50	Gln	Leu	Ala	Ser	Phe 55	Tyr	Ser	Phe	Leu	Val 60	Gly	Glu	Leu	Trp	
Pro 65	Arg	Gly	Arg	Asp	Gln 70	Trp	Glu	Ile	Phe	Leu 75	Glu	His	Val	Glu	Gln 80	
Leu	Ile	Asn	Gln	Gln 85	Ile	Thr	Glu	Asn	Ala 90	Arg	Asn	Thr	Ala	Leu 95	Ala	
Arg	Leu	Gln	Gly 100	Leu	Gly	Asp	Ser	Phe 105	Arg	Ala	Tyr	Gln	Gln 110	Ser	Leu	
Glu	Asp	Trp 115	Leu	Glu	Asn		Asp 120	Asp	Ala	Arg	Thr	Arg 125	Ser	Val	Leu	

Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro 130 135 140

- Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala 145

 Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe 165

 Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu 180
- Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp
 195 200 205
- Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp 210 215 220
- Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp 225 230 235 240
- Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn 245 250 255
- Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala -260 265 270
- Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro 275 280 285
- Ser Phe Ser Ala Ile Glu Ala Ala Ile Arg Ser Pro His Leu Leu 290 295 300
- Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser 305 310 315 320
- Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg 325 330 335
- Pro Ile Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr 340 345 350
- Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg 355 360 365
- Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro 370 375 380
- Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn 385 390 395 400
- Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro
 405 410 415
- Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr 420 425 430
- Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly
 435
 440
 445
- Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His 450 455 460
- Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

465					470					475					480
Ile	Pro	Met	Val	Lys 485	Ala	Ser	Glu	Leu	Pro 490	Gln	Gly	Thr	Thr	Val 495	Val
Arg	Gly	Pro	Gly 500	Phe	Thr	Gly	Gly	Asp 505	Ile	Leu	Arg	Arg	Thr 510	Asn	Thr
Gly	Gly	Phe 515	Gly	Pro	Ile	Arg	Val 520	Thr	Val	Asn	Gly	Pro 525	Leu	Thr	Gln
Arg	Туг 530	Arg	Ile	Gly	Phe	Arg 535	Tyr	Ala	Ser	Thr	Val 540	Asp	Phe	Asp	Phe
Phe 545	Val	Ser	Arg	Gly	Gly 550	Thr	Thr	Val	Asn	Asn 555	Phe	Arg	Phe	Leu	Arg 560
Thr	Met	Asn	Ser	Gly 565	Asp	Glu	Leu	Lys	Tyr 570	Gly	Asn	Phe	Val	Arg 575	Arg
Ala	Phe	Thr	Thr 580	Pro	Phe	Thr	Phe	Thr 585	Gln	Ile	Gln	Asp	Ile 590	Ile	Arg
Thr	Ser	Ile 595	Gln	Gly	Leu	Ser	Gly 600	Asn	Gly	Glu	Val	Tyr 605	Ile	Asp	Lys
Ile	Glu 610	Ile	Ile	Pro	Val	Thr 615	Ala	Thr	Phe	Glu	Ala 620	Glu	Tyr	Asp	Leu
Glu 625	Arg	Ala	Gln	Glu	Ala 630	Val	Asn	Ala	Leu	Phe 635	Thr	Asn	Thr	Asn	Pro 640
Arg	Arg	Leu	Lys	Thr 645	Asp	Val	Thr	qaA	Tyr 650	His	Ile	Asp	Gln	Val 655	Ser
Asn	Leu	Val	Ala 660	Cys	Leu	Ser	Asp	Glu 665	Phe	Cys	Leu	Asp	Glu 670	Lys	Arg
Glu	Leu	Leu 675	Glu	Lys	Val	Lys	Tyr 680	Ala	Lys	Arg	Leu	Ser 685	Asp	Glu	Arg
Asn	Leu 690	Leu	Gln	Asp	Pro	Asn 695	Phe	Thr	Ser	Ile	Asn 700	Lys	Gln	Pro	Asp
Phe 705	Ile	Ser	Thr	Asn	Glu 710	Gln	Ser	Asn	Phe	Thr 715	Ser	Ile	His	Glu	Gln 720
Ser	Glu	His	Gly	Trp 725	Trp	Gly	Ser	Glu	Asn 730	Ile	Thr	Ile	Gln	Glu 735	Gly
Asn	Asp	Val	Phe 740	Lys	Glu	Asn	Tyr	Val 745	Thr	Leu	Pro	Gly	Thr 750	Phe	Asn

Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln 770 Leu Glu Glu Ile Tyr Leu 790 Leu 790 Leu 795 Leu 795 Leu 795 Leu 790 Tyr Asn Ala Lys His Glu Thr Leu 800

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu 755 760 765

- Asp Val Pro Gly Thr Glu Ser Leu Trp Pro Leu Ser Val Glu Ser Pro 805 810 815
- Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp 820 825 830
- Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His 835 840 845
- His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu 850 855 860
- His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu 865 870 875 880
- Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu 885 890 895
- Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg 900 905 910
- Asp Lys Arg-Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu 915 920 925
- Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg 930 935 940
- Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu 945 950 955 960
- Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro 965 970 975
- Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr 980 985 990
- Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe 995 1000 1005
- Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln 1010 1015 1020
- Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu 1025 1030 1035 1040
- Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg 1045 1050 1055
- Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1060 1065 1070
- Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu
 1075 1080 1085
- Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala 1090 1095 1100
- His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala 1105 1110 1115 1120

Gly	Tyr	Glu	Asp	Ala 1125	_	Glu	Val	Asp	Thr 1130	Ala	Ser	Val	Asn 1135	
									_	-	_	_	_	_

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn 1140 1145 1150

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala 1155 1160 1165

Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val 1170 1180

Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val 1185 1190 1195 1200

Glu Leu Leu Met Glu Glu 1205

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

1275

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3465
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, partially maize optimized cryIA(b)" /note= "Disclosed in Figure 7 as contained in pCIB4434."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

			Asn		ATC Ile		Glu				Asn		48
Ser		Pro			GTG Val 1230	Leu				Ile			96
	Thr				AGC Ser				Gln				144
				Ala	GGC Gly			Gly				Ile	192
					AGC Ser								240

1285

1280

GAG CAG CTG ATC Glu Gln Leu Ile 1290	Asn Gln Arg I	TC GAG GAG TTC le Glu Glu Phe 295	C GCC CGC AAC e Ala Arg Asn 1300	CAG GCC 288 Gln Ala
ATC AGC CGC CTG Ile Ser Arg Leu 1305	GAG GGC CTG AG Glu Gly Leu Sc 1310	GC AAC CTG TAC er Asn Leu Tyi	C CAA ATC TAC r Gln Ile Tyr 1315	GCC GAG 336 Ala Glu
AGC TTC CGC GAG Ser Phe Arg Glu 1320	TGG GAG GCC G Trp Glu Ala A 1325	AC CCC ACC AAC sp Pro Thr Asi 133	n Pro Ala Leu	CGC GAG 384 Arg Glu 1335
GAG ATG CGC ATC Glu Met Arg Ile	CAG TTC AAC G Gln Phe Asn A 1340	AC ATG AAC AGG sp Met Asn Sei 1345	C GCC CTG ACC r Ala Leu Thr	ACC GCC 432 Thr Ala 1350
ATC CCC CTG TTC Ile Pro Leu Phe 135	Ala Val Gln A	AC TAC CAG GTO sn Tyr Gln Val 1360	G CCC CTG CTG l Pro Leu Leu 1365	Ser Val
TAC GTG CAG GCC Tyr Val Gln-Ala 1370	Ala Asn Leu H	AC CTG AGC GTG is Leu Ser Val 375	G CTG CGC GAC l Leu Arg Asp 1380	GTC AGC 528 Val Ser
GTG TTC GGC CAG Val Phe Gly Gln 1385	CGC TGG GGC T Arg Trp Gly P 1390	TC GAC GCC GCC he Asp Ala Ala	a Thr Ile Asn	AGC CGC 576 Ser Arg
TAC AAC GAC CTG Tyr Asn Asp Leu 1400	ACC CGC CTG A Thr Arg Leu I 1405	TC GGC AAC TAG le Gly Asn Ty: 14:	r Thr Asp His	GCC GTG 624 Ala Val 1415
CGC TGG TAC AAC Arg Trp Tyr Asn	ACC GGC CTG G. Thr Gly Leu G 1420	AG CGC GTG TGC lu Arg Val Trp 1425	G GGT CCC GAC p Gly Pro Asp	AGC CGC 672 Ser Arg 1430
GAC TGG ATC AGG Asp Trp Ile Arg 143	Tyr Asn Gln P	TC CGC CGC GAG he Arg Arg Glu 1440	G CTG ACC CTG u Leu Thr Leu 1445	Thr Val
CTG GAC ATC GTG Leu Asp Ile Val 1450	Ser Leu Phe P	CC AAC TAC GA(ro Asn Tyr As) 455	C AGC CGC ACC p Ser Arg Thr 1460	TAC CCC 768 Tyr Pro
ATC CGC ACC GTG Ile Arg Thr Val 1465	AGC CAG CTG A Ser Gln Leu T 1470	CC CGC GAG AT hr Arg Glu Ilo	T TAC ACC AAC e Tyr Thr Asn 1475	CCC GTG 816 Pro Val
CTG GAG AAC TTC Leu Glu Asn Phe 1480	GAC GGC AGC T Asp Gly Ser P 1485	TC CGC GGC AGG he Arg Gly Se: 14	r Ala Gln Gly	ATC GAG 864 Ile Glu 1495
GGC AGC ATC CGC Gly Ser Ile Arg	AGC CCC CAC C Ser Pro His L 1500	TG ATG GAC ATG eu Met Asp Ilo 1505	C CTG AAC AGC e Leu Asn Ser	ATC ACC 912 Ile Thr 1510
ATC TAC ACC GAC Ile Tyr Thr Asp 151	Ala His Arg G	GC GAG TAC TAC ly Glu Tyr Ty: 1520	C TGG AGC GGC r Trp Ser Gly 1525	His Gln

ATC ATG GCC AGC Ile Met Ala Ser 1530	CCC GTC GGC Pro Val Gly	TTC AGC GGC Phe Ser Gly 1535	CCC GAG TTC Pro Glu Phe 1540	Thr Phe Pro	1008
CTG TAC GGC ACC Leu Tyr Gly Thr 1545	ATG GGC AAC Met Gly Asn 1550	Ala Ala Pro	CAG CAG CGC Gln Gln Arg 1555	ATC GTG GC	A 1056 a
CAG CTG GGC CAG Gln Leu Gly Gln 1560	GGA GTG TAC Gly Val Tyr 1565	CGC ACC CTG Arg Thr Leu	AGC AGC ACC Ser Ser Thr 1570	CTG TAC CG Leu Tyr Ar	g
CGA CCT TTC AAC Arg Pro Phe Asn	ATC GGC ATC Ile Gly Ile 1580	AAC AAC CAG Asn Asn Gln 158	Gln Leu Ser	GTG CTG GA Val Leu As 1590	C 1152
GGC ACC GAG TTC Gly Thr Glu Phe 159	Ala Tyr Gly	ACC AGC AGC Thr Ser Ser 1600	AAC CTG CCC Asn Leu Pro	AGC GCC GT Ser Ala Va 1605	G 1200 1
TAC CGC AAG AGC Tyr Arg Lys Ser 1610	GGC ACC GTG Gly Thr Val	GAC AGC CTG Asp Ser Leu 1615	GAC GAG ATC Asp Glu Ile 1620	Pro Pro GI	G 1248 n
AAC AAC AAC GTG Asn Asn Asn Val 1625	CCA CCT CGA Pro Pro Arg 163	Gln Gly Phe	AGC CAC CGT Ser His Arg 1635	CTG AGC CA Leu Ser Hi	C 1296 s
GTG AGC ATG TTC Val Ser Met Phe 1640	CGC AGT GGC Arg Ser Gly 1645	TTC AGC AAC Phe Ser Asr	AGC AGC GTG Ser Ser Val 1650	AGC ATC AT Ser Ile Il 16	e
CGT GCA CCT ATG Arg Ala Pro Met	TTC AGC TGG Phe Ser Trp 1660	ATT CAC CGC Ile His Arg 166	Ser Ala Glu	TTC AAC AA Phe Asn As 1670	C 1392 n
ATC ATC CCC AGC Ile Ile Pro Ser 167	Ser Gln Ile	ACC CAG ATO Thr Gln Ile 1680	C CCC CTG ACC Pro Leu Thr	AAG AGC AC Lys Ser Th 1685	C 1440 r
AAC CTG GGC AGC Asn Leu Gly Ser 1690	GGC ACC AGC Gly Thr Ser	GTG GTG AAC Val Val Lys 1695	G GGC CCC GGC G Gly Pro Gly 170	Phe Thr GI	С 1488 У
GGC GAC ATC CTG Gly Asp Ile Leu 1705	CGC CGC ACC Arg Arg Thr 171	Ser Pro Gly	C CAG ATC AGC Gln Ile Ser 1715	ACC CTG CG Thr Leu Ar	c 1536 g
GTG AAC ATC ACC Val Asn Ile Thr 1720	GCC CCC CTG Ala Pro Leu 1725	AGC CAG CGC Ser Gln Arg	TAC CGC GTC Tyr Arg Val 1730	Arg Ile Ar	g 1584 g 35
TAC GCC AGC ACC Tyr Ala Ser Thr	ACC AAC CTG Thr Asn Leu 1740	CAG TTC CAG Gln Phe His	s Thr Ser Ile	GAC GGC CG Asp Gly Ar 1750	c 1632
CCC ATC AAC CAG Pro Ile Asn Glr 175	Gly Asn Phe	AGC GCC ACC Ser Ala Thi 1760	C ATG AGC AGC r Met Ser Ser	GGC AGC AA Gly Ser As 1765	C 1680
CTG CAG AGC GGC	AGC TTC CGC	ACC GTG GGG	C TTC ACC ACC	CCC TTC AA	AC 1728

Leu Gln Ser Gly Ser 1770	r Phe Arg Thr Val 1775	. Gly Phe Thr Thr I	Pro Phe Asn
TTC AGC AAC GGC AG Phe Ser Asn Gly Se 1785	C AGC GTG TTC ACC r Ser Val Phe Thi 1790	C CTG AGC GCC CAC G Leu Ser Ala His V 1795	TTG TTC AAC 1776 Val Phe Asn
AGC GGC AAC GAG GT	G TAC ATC GAC CGG	C ATC GAG TTC GTG C	CCC GCC GAG 1824
Ser Gly Asn Glu Va	l Tyr Ile Asp Arg	g Ile Glu Phe Val I	Pro Ala Glu
1800	1805	1810	1815
GTG ACC TTC GAG GC	a Glu Tyr Asp Le	G GAG AGG GCT CAG A	AAG GCC GTG 1872
Val Thr Phe Glu Al		1 Glu Arg Ala Gln I	Lys Ala Val
18		1825	1830
AAC GAG CTG TTC AC	C AGC AGC AAC CA	n Ile Gly Leu Lys	ACC GAC GTG 1920
Asn Glu Leu Phe Th	r Ser Ser Asn Gli		Thr Asp Val
1835	18		1845
ACC GAC TAC CAC AT Thr Asp Tyr His II 1850	C GAT CAA GTA TC e Asp Gln Val Se 1855	C AAT TTA GTT GAG ? r Asn Leu Val Glu (1860	TGT TTA TCT 1968 Cys Leu Ser
GAT GAA TTT TGT CT Asp Glu Phe Cys Le 1865	G GAT GAA AAA AA u Asp Glu Lys Ly 1870	A GAA TTG TCC GAG A s Glu Leu Ser Glu 1 1875	AAA GTC AAA 2016 Lys Val Lys
CAT GCG AAG CGA CT	T AGT GAT GAG CG	G AAT TTA CTT CAA 0	GAT CCA AAC 2064
His Ala Lys Arg Le	u Ser Asp Glu Ar	g Asn Leu Leu Gln 1	Asp Pro Asn
1880	1885	1890	1895
TTT AGA GGG ATC APPhe Arg Gly Ile As	T AGA CAA CTA GA	C CGT GGC TGG AGA	GGA AGT ACG 2112
	n Arg Gln Leu As	p Arg Gly Trp Arg	Gly Ser Thr
	00	1905	1910
GAT ATT ACC ATC CAR Asp Ile Thr Ile GI 1915	n Gly Gly Asp As	p Val Phe Lys Glu .	AAT TAC GTT 2160 Asn Tyr Val 1925
ACG CTA TTG GGT ACT Thr Leu Leu Gly The 1930	C TTT GAT GAG TG ir Phe Asp Glu Cy 1935	C TAT CCA ACG TAT s Tyr Pro Thr Tyr 1940	Leu Tyr Gin
AAA ATA GAT GAG TO Lys Ile Asp Glu So 1945	CG AAA TTA AAA GC er Lys Leu Lys Al 1950	C TAT ACC CGT TAC a Tyr Thr Arg Tyr 1955	CAA TTA AGA 2256 Gln Leu Arg
GGG TAT ATC GAA G	AT AGT CAA GAC TI	TA GAA ATC TAT TTA	ATT CGC TAC 2304
Gly Tyr Ile Glu A	sp Ser Gln Asp Le	Eu Glu Ile Tyr Leu	Ile Arg Tyr
1960	1965	1970	1975
Asn Ala Lys His G	AA ACA GTA AAT GT	CG CCA GGT ACG GGT	TCC TTA TGG 2352
	Lu Thr Val Asn Va	al Pro Gly Thr Gly	Ser Leu Trp
	980	1985	1990
CCG CTT TCA GCC C Pro Leu Ser Ala P 1995	co Ser Pro Ile G	GA AAA TGT GCC CAT Ly Lys Cys Ala His	CAT TCC CAT 2400 His Ser His 2005
CAT TTC TCC TTG G	AC ATT GAT GTT GG	GA TGT ACA GAC TTA	AAT GAG GAC 2448
His Phe Ser Leu A	sp Ile Asp Val G	Ly Cys Thr Asp Leu	Asn Glu Asp

2010 2015 2020

TTA GGT GTA TGG GTG ATA Leu Gly Val Trp Val Ile 2025	TTC AAG ATT AA Phe Lys Ile Ly 2030	G ACG CAA GAT GGC s Thr Gln Asp Gly 2035	CAT GCA 2496 His Ala
AGA CTA GGA AAT CTA GAA	Phe Leu Glu Gl	G AAA CCA TTA GTA	GGA GAA 2544
Arg Leu Gly Asn Leu Glu		u Lys Pro Leu Val	Gly Glu
2040 2045		2050	2055
GCA CTA GCT CGT GTG AAA	AGA GCG GAG AA	s Lys Trp Arg Asp	AAA CGT 2592
Ala Leu Ala Arg Val Lys	Arg Ala Glu Ly		Lys Arg
2060	20		2070
GAA AAA TTG GAA TGG GAA	ACA AAT ATT GT	T TAT AAA GAG GCA	Lys Glu
Glu Lys Leu Glu Trp Glu	Thr Asn Ile Va	l Tyr Lys Glu Ala	
2075	2080	208	
TCT GTA GAT GCT TTA TTT Ser Val Asp Ala Leu Phe 2090	GTA AAC TCT CA Val Asn Ser Gl 2095	A TAT GAT AGA TTA n Tyr Asp Arg Leu 2100	CAA GCG 2688 Gln Ala
GAT ACC AAC ATC GCG ATG Asp Thr Asn Ile Ala Met 2105	ATT CAT GCG GC Ile His Ala Al 2110	A GAT AAA CGC GTT a Asp Lys Arg Val 2115	CAT AGC 2736 His Ser
ATT CGA GAA GCT TAT CTG Ile Arg Glu Ala Tyr Leu 2120 212	Pro Glu Leu Se	T GTG ATT CCG GGT r Val Ile Pro Gly 2130	GTC AAT 2784 .Val Asn 2135
GCG GCT ATT TTT GAA GAA	Leu Glu Gly Ar	T ATT TTC ACT GCA	TTC TCC 2832
Ala Ala Ile Phe Glu Glu		g Ile Phe Thr Ala	Phe Ser
2140		45	2150
CTA TAT GAT GCG AGA AAT	GTC ATT AAA AA	T GGT GAT TTT AAT	Asn Gly
Leu Tyr Asp Ala Arg Asn	Val Ile Lys As	n Gly Asp Phe Asn	
2155	2160	216	
TTA TCC TGC TGG AAC GTG Leu Ser Cys Trp Asn Val 2170	AAA GGG CAT GT Lys Gly His Va 2175	A GAT GTA GAA GAA 1 Asp Val Glu Glu 2180	CAA AAC 2928 Gln Asn
AAC CAC CGT TCG GTC CTT Asn His Arg Ser Val Leu 2185	GTT GTT CCG GAVAL Val Val Pro GI	AA TGG GAA GCA GAA u Trp Glu Ala Glu 2195	GTG TCA 2976 Val Ser
CAA GAA GTT CGT GTC TGT	Pro Gly Arg G	GC TAT ATC CTT CGT	GTC ACA 3024
Gln Glu Val Arg Val Cys		Ly Tyr Ile Leu Arg	Val Thr
2200 220		2210	2215
GCG TAC AAG GAG GGA TAT	Gly Glu Gly Cy	GC GTA ACC ATT CAT	GAG ATC 3072
Ala Tyr Lys Glu Gly Tyr		ys Val Thr Ile His	Glu Ile
2220		225	2230
GAG AAC AAT ACA GAC GAA	CTG AAG TTT AG	GC AAC TGT GTA GAA	. Glu Glu
Glu Asn Asn Thr Asp Glu	Leu Lys Phe So	er Asn Cys Val Glu	
2235	2240	224	
GTA TAT CCA AAC AAC ACG Val Tyr Pro Asn Asn Thr 2250	GTA ACG TGT A Val Thr Cys A 2255	AT GAT TAT ACT GCG sn Asp Tyr Thr Ala 2260	ACT CAA 3168 Thr Gln

		Tyr					Thr					Gly		GAC Asp	_	3216
_	Tyr				-	Ser		-	-		Tyr	_		GCC Ala		3264
					Thr					Asp				GAA Glu 2310	Ser	3312
				Gly					Leu					GTG Val		3360
			Glu					Thr					Ile	GAG Glu	_	3408
		Thr					Ile					Glu		CTT Leu		3456
_	GAG Glu)		TAA											4		3468

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

- Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
- Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140
- Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
- Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175
- Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
- Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205
- Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220
- Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240
- Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255
- Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270
- Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285
- Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300
- Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315 320
- Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335
- Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350
- Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365
- Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380
- Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400
- Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415
- Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 455 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 470 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 490 485 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 505 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 520 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 555 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 570 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 590 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 650 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 715 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr

755 760 765

Asn	Ala 770	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro 785	Leu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Ala	His	His	Ser	His 800
His	Phe	Ser	Leu	Asp 805	Ile	Asp	Val	Gly	Cys 810	Thr	Asp	Leu	Asn	Glu 815	Asp
Leu	Gly	Val	Trp 820	Val	Ile	Phe	Lys	Ile 825	Lys	Thr	Gln	Asp	Gly 830	His	Ala
Arg	Leu	Gly 835	Asn	Leu	Glu	Phe	Leu 840	Glu	Glu	Lys	Pro	Leu 845	Val	Gly	Glu
Ala	Leu 850	Ala	Arg	Val	Lys	Arg 855	Ala	Glu	Lys	Lys	Trp 860	Arg	Asp	Lys	Arg
Glu 865	Lys	Leu	Glu	Trp	Glu 870	Thr	Asn	Ile	Val	Tyr 875	Lys	Glu	Ala	Lys	Glu 880
Ser	Val	Asp	Ala	Leu 885	Phe	Val	Asn	Ser	Gln 890	Tyr	Asp	Arg	Leu	Gln 895	Ala
Asp	Thr	Asn	Ile 900	Ala	Met	Ile	His	Ala 905	Ala	Asp	Lys	Arg	Val 910	His	Ser
Ile	Arg	Glu 915	Ala	Tyr	Leu	Pro	Glu 920	Leu	Ser	Val	Ile	Pro 925	Gly	Val	Asn
Ala	Ala 930	Ile	Phe	Glu	Glu	Leu 935	Glu	Gly	Arg	Ile	Phe 940	Thr	Ala	Phe	Ser
Leu 945	Tyr	Asp	Ala	Arg	Asn 950	Val	Ile	Lys	Asn	Gly 955	Asp	Phe	Asn	Asn	Gly 960
Leu	Ser	Cys	Trp	Asn 965	Val	Lys	Gly	His	Val 970	Asp	Val	Glu	Glu	Gln 975	Asn
Asn	His	Arg	Ser 980	Val	Leu	Val	Val	Pro 985	Glu	Trp	Glu	Ala	Glu 990	Val	Ser
Gln	Glu	Val 995	Arg	Val	Cys	Pro	Gly 100	Arg O	Gly	Tyr	Ile	Leu 100	Arg 5	Val	Thr
Ala	Tyr 101		Glu	Gly	Tyr	Gly 101		Gly	Cys	Val	Thr 102	Ile O	His	Glu	Ile
Glu 102		Asn	Thr	Asp	Glu 103		Lys	Phe	Ser	Asn 103	Cys 5	Val	Glu	Glu	Glu 1040
Val	Tyr	Pro	Asn	Asn 104		Val	Thr	Cys	Asn 105	Asp 0	Tyr	Thr	Ala	Thr 105	Gln 5
Glu	Glu	Tyr	Glu 106		Thr	Tyr	Thr	Ser 106		Asn	Arg	Gly	Tyr 107	Asp 0	Gly
Ala	Tyr	Glu 107		Asn	Ser	Ser	Val 108		Ala	Asp	Tyr	Ala 108	Ser 5	Ala	Tyr

Glu	Glu	Lys	Ala	Tyr	Thr	Asp	Gly	Arg	Arg	Asp	Asn	Pro	Cys	Glu	Ser
	1090			_		1095					1100				

Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr 1105 1110 1115 1120

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile 1125 1130 1135

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu 1140 1145 1150

Met Glu Glu 1155

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
 - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)" /note= "Disclosed in Figure 9 as contained in pCIB5511."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG Met	GAC Asp	AAC Asn	AAC Asn	CCC Pro 1160	Asn	ATC Ile	AAC Asn	GAG Glu	TGC Cys 1165	Ile	CCC Pro	TAC Tyr	AAC Asn	TGC Cys 1170	Leu	48
AGC Ser	AAC Asn	CCC Pro	GAG Glu 1175	Val	GAG Glu	GTG Val	CTG Leu	GGC Gly 1180	Gly	GAG Glu	CGC Arg	ATC Ile	GAG Glu 118	ACC Thr	GGC Gly	96
TAC Tyr	ACC Thr	CCC Pro 1190	Ile	GAC Asp	ATC Ile	AGC Ser	CTG Leu 1195	Ser	CTG Leu	ACC Thr	CAG Gln	TTC Phe 1200	Leu	CTG Leu	AGC Ser	144
GAG Glu	TTC Phe 120	Val	CCC Pro	GGC Gly	GCC Ala	GGC Gly 121	Phe	GTG Val	CTG Leu	GGC Gly	CTG Leu 121	GTG Val	GAC Asp	ATC Ile	ATC Ile	192

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

1220 1225 1230 1235

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC 288

Glu Gln Leu	Ile Asn Gln 1240	Arg Ile Gl	u Glu Phe 1 1245	Ala Arg Asn	Gln Ala 1250
ATC AGC CGC Ile Ser Arg	CTG GAG GGC Leu Glu Gly 1255	Leu Ser As	AC CTG TAC (sn Leu Tyr (260	CAA ATC TAC Gln Ile Tyr 1265	Ala Glu
AGC TTC CGC Ser Phe Arg 127	GAG TGG GAG Glu Trp Glu)	GCC GAC CC Ala Asp Pr 1275	CC ACC AAC ro Thr Asn	CCC GCC CTG Pro Ala Leu 1280	CGC GAG 384 Arg Glu
GAG ATG CGC Glu Met Arg 1285	ATC CAG TTC Ile Gln Phe	AAC GAC AT Asn Asp Me 1290	et Asn Ser	GCC CTG ACC Ala Leu Thr 1295	ACC GCC 432 Thr Ala
ATC CCC CTG Ile Pro Leu 1300	TTC GCC GTG Phe Ala Val 130	Gln Asn Ty	AC CAG GTG yr Gln Val 1310	Pro Leu Leu	AGC GTG 480 Ser Val 1315
TAC GTG CAG Tyr Val Gln	GCC GCC AAC Ala Ala Asn 1320	CTG CAC CT Leu His Le	TG AGC GTG eu Ser Val 1325	CTG CGC GAC Leu Arg Asp	GTC AGC 528 Val Ser 1330
GTG TTC GGC Val Phe Gly	CAG CGC TGG Gln Arg Trp 1335	Gly Phe As	AC GCC GCC sp Ala Ala 340	ACC ATC AAC Thr Ile Asn 1345	Ser Arg
TAC AAC GAC Tyr Asn Asp 135	CTG ACC CGC Leu Thr Arg 0	CTG ATC GG Leu Ile Gl 1355	GC AAC TAC ly Asn Tyr	ACC GAC CAC Thr Asp His 1360	GCC GTG 624 Ala Val
CGC TGG TAC Arg Trp Tyr 1365	AAC ACC GGC Asn Thr Gly	CTG GAG CO Leu Glu Ar 1370	GC GTG TGG rg Val Trp	GGT CCC GAC Gly Pro Asp 1375	AGC CGC 672 Ser Arg
GAC TGG ATO Asp Trp Ile 1380	AGG TAC AAC Arg Tyr Asn 138	Gln Phe Ar	GC CGC GAG rg Arg Glu 1390	Leu Thr Leu	ACC GTG 720 Thr Val 1395
CTG GAC ATO	GTG AGC CTG Val Ser Leu 1400	TTC CCC A	AC TAC GAC sn Tyr Asp 1405	AGC CGC ACC Ser Arg Thr	TAC CCC 768 Tyr Pro 1410
ATC CGC ACC	C GTG AGC CAG Val Ser Glr 1415	ı Leu Thr Ai	GC GAG ATT arg Glu Ile .420	TAC ACC AAC Tyr Thr Asn 142	Pro Val
CTG GAG AAC Leu Glu Asr 143	C TTC GAC GGO n Phe Asp Gly	C AGC TTC CO y Ser Phe A: 1435	GC GGC AGC Arg Gly Ser	GCC CAG GGC Ala Gln Gly 1440	ATC GAG 864 Ile Glu
GGC AGC ATC Gly Ser Ile 1445	C CGC AGC CCC e Arg Ser Pro	C CAC CTG A' O His Leu M 1450	ATG GAC ATC Met Asp Ile	CTG AAC AGC Leu Asn Ser 1455	ATC ACC 912 Ile Thr
ATC TAC ACC Ile Tyr Thi 1460	C GAC GCC CAC r Asp Ala His 140	s Arg Gly G	GAG TAC TAC Glu Tyr Tyr 1470	Trp Ser Gly	CAC CAG 960 His Gln 1475
ATC ATG GCG	C AGC CCC GTO a Ser Pro Vai	C GGC TTC A l Gly Phe S	AGC GGC CCC Ser Gly Pro	GAG TTC ACC	TTC CCC 1008 Phe Pro

1480 1485 1490

CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1495 1500 1505	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1510 1515 1520	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1525 1530 1535	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1540 1545 1550	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1560 1565 1570	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1575 1580 1585	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1590 1595 1600	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1605 1610 1615	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1620 1625 1630 1635	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1640 1645 1650	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1655 1660 1665	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1670 1675 1680	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1685 1690 1695	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1700 1705 1710 1715	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1720 1725 1730	1728

TTC AGC AAC GGC Phe Ser Asn Gly 173	Ser Ser Val				
AGC GGC AAC GAG Ser Gly Asn Glu 1750				Pro Ala	
GTG ACC TTC GAG Val Thr Phe Glu 1765		Asp Leu Glu			
AAC GAG CTG TTC Asn Glu Leu Phe 1780					
ACC GAC TAC CAC Thr Asp Tyr His			Leu Val Glu		Ser
GAT GAA TTT TGT Asp Glu Phe Cys 181	Leu Asp Glu				
CAT GCG AAG CGA His Ala Lys Arg 1830				Asp Pro	
TTT AGA GGG ATC Phe Arg Gly Ile 1845		Leu Asp Arg			
GAT ATT ACC ATC Asp Ile Thr Ile 1860					
ACG CTA TTG GGT Thr Leu Leu Gly			Pro Thr Tyr		Gln
AAG ATC GAC GAG Lys Ile Asp Glu 189	Ser Lys Leu				
GGC TAC ATC GAG Gly Tyr Ile Glu 1910				Ile Arg	
AAC GCC AAG CAC Asn Ala Lys His 1925		Asn Val Pro			
CCC CTG AGC GCC Pro Leu Ser Ala 1940					
TGC GCT CCG CAC Cys Ala Pro His			Leu Asp Cys		Arg

GAC Asp	GGG Gly	GAG Glu	AAG Lys 1975	Cys	GCC Ala	CAC His	CAC His	AGC Ser 1980	His	CAC His	TTC Phe	AGC Ser	CTG Leu 1985	Asp	ATC Ile	2496
GAC Asp	GTG Val	GGC Gly 1990	Cys	ACC Thr	GAC Asp	CTG Leu	AAC Asn 1995	GAG Glu	GAC Asp	CTG Leu	GGC Gly	GTG Val 2000	Trp	GTG Val	ATC Ile	2544
TTC Phe	AAG Lys 2005	Ile	AAG Lys	ACC Thr	CAG Gln	GAC Asp 2010	Gly	CAC His	GCC Ala	CGC Arg	CTG Leu 2015	Gly	AAT Asn	CTA Leu	GAA Glu	2592
TTT Phe 2020	Leu	GAA Glu	GAG Glu	AAA Lys	CCA Pro 2025	Leu	GTA Val	GGA Gly	GAA Glu	GCA Ala 2030	Leu	GCT Ala	CGT Arg	GTG Val	AAA Lys 2035	2640
AGA Arg	GCG Ala	GAG Glu	AAA Lys	AAA Lys 2040	Trp	AGA Arg	GAC Asp	AAA Lys	CGT Arg 2045	Glu	AAA Lys	TTG Leu	GAA Glu	TGG Trp 2050	Glu	2688
ACA Thr	AAT Asn	Ile	GTT Val 2055	Tyr	AAA Lys	GAG Glu	GCA Ala	AAA Lys 2060	Glu	TCT Ser	GTA Val	GAT Asp	GCT Ala 2065	Leu	TTT Phe	2736
GTA Val	AAC Asn	TCT Ser 2070	Gln	TAT Tyr	GAT Asp	AGA Arg	TTA Leu 2075	CAA Gln	GCG Ala	GAT Asp	ACC Thr	AAC Asn 2080	Ile	GCG Ala	ATG Met	2784
ATT Ile	CAT His 2085	Ala	GCA Ala	GAT Asp	AAA Lys	CGC Arg 2090	Val	CAT His	AGC Ser	ATT Ile	CGA Arg 2095	Glu	GCT Ala	TAT Tyr	CTG Leu	2832
CCT Pro 2100	Glu	CTG Leu	TCT Ser	GTG Val	ATT Ile 2105	Pro	GGT Gly	GTC Val	AAT Asn	GCG Ala 2110	Ala	ATT Ile	TTT Phe	GAA Glu	GAA Glu 2115	2880
TTA Leu	GAA Glu	GGG Gly	CGT Arg	ATT Ile 2120	Phe	ACT Thr	GCA Ala	TTC Phe	TCC Ser 2125	Leu	TAT Tyr	GAT Asp	GCG Ala	AGA Arg 2130	Asn	2928
GTC Val	ATT Ile	AAA Lys	AAT Asn 2135	Gly	GAT Asp	TTT Phe	AAT Asn	AAT Asn 2140	Gly	TTA Leu	TCC Ser	TGC Cys	TGG Trp 2145	Asn	GTG Val	2976
AAA Lys	GGG Gly	CAT His 215	Val	GAT Asp	GTA Val	GAA Glu	GAA Glu 215	CAA Gln 5	AAC Asn	AAC Asn	CAC His	CGT Arg 2160	Ser	GTC Val	CTT Leu	3024
GTT Val	GTT Val 2165	Pro	GAA Glu	TGG Trp	GAA Glu	GCA Ala 2170	Glu	GTG Val	TCA Ser	CAA Gln	GAA Glu 217	Val	CGT Arg	GTC Val	TGT Cys	3072
CCG Pro 2180	Gly	CGT Arg	GGC Gly	TAT Tyr	ATC Ile 218	Leu	CGT Arg	GTC Val	ACA Thr	GCG Ala 2190	Tyr	AAG Lys	GAG Glu	GGA Gly	TAT Tyr 2195	3120
GGA Gly	GAA Glu	GGT Gly	TGC Cys	GTA Val 220	Thr	ATT Ile	CAT His	GAG Glu	ATC Ile 220	Glu	AAC Asn	AAT Asn	ACA Thr	GAC Asp 221	Glu	3168
CTG	AAG	TTT	AGC	AAC	TGT	GTA	GAA	GAG	GAA	GTA	TAT	CCA	AAC	AAC	ACG	3216

	Lys	Phe	Ser 2215		Cys	Val	Glu	Glu 2220	Glu	Val	Tyr	Pro	Asn 2225	Asn	Thr	
GTA Val	ACG Thr	TGT Cys 2230	Asn	GAT Asp	TAT Tyr	ACT Thr	GCG Ala 2235	ACT Thr	CAA Gln	GAA Glu	GAA Glu	TAT Tyr 2240	Glu	GGT Gly	ACG Thr	3264
TAC Tyr	ACT Thr 2245	Ser	CGT Arg	AAT Asn	CGA Arg	GGA Gly 2250	Tyr	GAC Asp	GGA Gly	GCC Ala	TAT Tyr 2255	Glu	AGC Ser	AAT Asn	TCT Ser	3312
TCT Ser 226	Val	CCA Pro	GCT Ala	GAT Asp	TAT Tyr 2265	Ala	TCA Ser	GCC Ala	TAT Tyr	GAA Glu 2270	Glu	AAA Lys	GCA Ala	TAT Tyr	ACA Thr 2275	3360
GAT Asp	GGA Gly	CGA Arg	AGA Arg	GAC Asp 228	Asn	CCT Pro	TGT Cys	GAA Glu	TCT Ser 2285	Asn	AGA Arg	GGA Gly	TAT Tyr	GGG Gly 229	Asp	3408
TAC Tyr	ACA Thr	CCA Pro	CTA Leu 229	Pro	GCT Ala	GGC Gly	TAT Tyr	GTG Val 2300	Thr	AAA Lys	GAA Glu	TTA Leu	GAG Glu 230	Tyr	TTC Phe	3456
CCA Pro	GAA Glu	ACC Thr 231	Asp	AAG Lys	GTA Val	TGG Trp	ATT Ile 231	GAG Glu 5	ATC Ile	GGA Gly	GAA Glu	ACG Thr 232	Glu	GGA Gly	ACA Thr	3504
TTC Phe	ATC Ile 232	Val	GAC Asp	AGC Ser	GTG Val	GAA Glu 233	Leu	CTT Leu	CTT Leu	ATG Met	GAG Glu 233	Glu	TAA	٠.		3546
(2)	INF	ORMA	TION	FOR	SEQ	ID :	NO:1	1:								
(2)			SEQU (A (B	ENCE) LE) TY	CHA	RACT: 11	ERIS 81 a o ac	TICS mino id	: aci	ds						
(2)		(i)	SEQU (A (B	ENCE) LE) TY) TO	CHA NGTH PE: POLO	RACT: : 11 amin GY:	ERIS 81 a o ac line	TICS mino id ar	: aci	ds						
(2)	((i) ii)	SEQU (A (B (D MOLE	ENCE) LE) TY) TO	CHA NGTH PE: POLO	RACT: : 11 amin GY: E: p	ERIS 81 a o ac line rote	TICS mino id ar	aci		11:					
) (: Asp	(i) ii) xi)	SEQU (A (B (D MOLE	ENCE) LE) TY) TO CULE	CHA NGTH PE: POLO TYP DES Asn	RACT: : 11 amin GY: E: p	ERIS 81 a o ac line rote TION	TICS mino id ar in	aci	NO:		Tyr	Asn	Cys 15	Leu	
Met 1) (: Asp	(i) ii) xi) Asn	SEQU (A (B (D MOLE SEQU Asn	ENCE) LE) TY) TO CULE ENCE Pro 5	CHA NGTH PE: POLO TYP DES Asn	RACT: : 11 amin GY: E: p CRIP	ERIS 81 a o ac line rote TION Asn	TICS mino id ar in	aci Q ID Cys 10 Gly	NO:	Pro			15 Thr		
Met 1 Ser	(: Asp	(i) ii) xi) Asn	SEQU (A (B (D MOLE SEQU Asn Glu 20	ENCE) LE) TY) TO CULE ENCE Pro 5	CHANGTH PE: POLO TYP DES Asn	RACT: : 11 amin GY: E: p CRIP Ile Val	ERIS 81 a o ac line rote TION Asn Leu	TICS mino id ar in : SE Glu Gly 25	aci Q ID Cys 10 Gly	NO: Ile Glu	Pro Arg	Ile	Glu 30	Thr	Gly	
Met 1 Ser Tyr	(Asp Asn	(i) ii) xi) Asn Pro Pro 35	SEQU (A (B (D MOLE SEQU Asn Glu 20	ENCE) LE) TY) TO CULE ENCE Pro 5 Val	CHANGTH PE: POLO TYP DES Asn Glu	RACT: : 11 amin GY: E: p CRIP Ile Val	ERIS 81 a o ac line rote TION Asn Leu 40	TICS mino id ar in : SE Glu Gly 25	aci Q ID Cys 10 Gly Leu	NO: Ile Glu	Pro Arg	Ile Phe 45	Glu 30	Thr Leu	Gly Ser	
Met 1 Ser Tyr	(() Asp Asn Thr Phe 50 Gly	(i) ii) xi) Asn Pro 35	SEQU (A (B (D MOLE SEQU Asn Glu 20 Ile	ENCE) LE) TY) TO CULE ENCE Pro 5 Val	CHANGTH PE: POLO TYP DES Asn Glu Ile	RACT: : 11 amin GY: E: p CRIP Ile Val Ser Gly 55	ERIS 81 a o ac line rote TION Asn Leu 40 Phe	TICS mino id ar in : SE Glu Gly 25	aci Q ID Cys 10 Gly Leu	NO: Ile Glu Thr	Pro Arg Gln Leu 60	Ile Phe 45 Val	Glu 30 Leu Asp	Thr Leu	Gly Ser Ile	

- Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110
- Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
- Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140
- Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
- Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175
- Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
- Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205
- Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220
- Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240
- Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255
- Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270
- Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285
- Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300
- Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315
- Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335
- Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350
- Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365
- Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380
- Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400
- Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415
- Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His

420 425 430

Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
Ile 465	Ile	Pro	Ser	Ser	Gln 470	Ile	Thr	Gln	Ile	Pro 475	Leu	Thr	Lys	Ser	Thr 480
Asn	Leu	Gly	Ser	Gly 485	Thr	Ser	Val	Val	Lys 490	Gly	Pro	Gly	Phe	Thr 495	Gly
Gly	Asp	Ile	Leu 500	Arg	Arg	Thr	Ser	Pro 505	Gly	Gln	Ile	Ser	Thr 510	Leu	Arg
Val	Asn	Ile 515	Thr	Ala	Pro	Leu	Ser 520	Gln	Arg	Tyr	Arg	Val 525	Arg	Ile	Arg
Tyr	Ala 530	Ser	Thr	Thr	Asn	Leu 535	Gln	Phe	His	Thr	Ser 540	Ile	Asp	Gly	Arg
Pro 545	Ile	Asn	Gln	Gly	Asn 550	Phe	Ser	Ala	Thr	Met 555	Ser	Ser	Gly	Ser	Asn 560
Leu	Gln	Ser	Gly	Ser 565	Phe	Arg	Thr	Val	Gly 570	Phe	Thr	Thr	Pro	Phe -575	Asn
Phe	Ser	Asn	Gly 580	Ser	Ser	Val	Phe	Thr 585	Leu	Ser	Ala	His	Val 590	Phe	Asn
Ser	Gly	Asn 595	Glu	Val	Tyr	Ile	Asp 600	Arg	Ile	Glu	Phe	Val 605	Pro	Ala	Glu
Val	Thr 610	Phe	Glu	Ala	Glu	Tyr 615	Asp	Leu	Glu	Arg	Ala 620	Gln	Lys	Ala	Val
Asn 625	Glu	Leu	Phe	Thr	Ser 630	Ser	Asn	Gln	Ile	Gly 635	Leu	Lys	Thr	Asp	Val 640
Thr	Asp	Tyr	His	Ile 645	Asp	Gln	Val	Ser	Asn 650	Leu	Val	Glu	Cys	Leu 655	Ser
Asp	Glu	Phe	Cys 660	Leu	Asp	Glu	Lys	Lys 665	Glu	Leu	Ser	Glu	Lys 670	Val	Lys
His	Ala	Lys 675	Arg	Leu	Ser	Asp	Glu 680	Arg	Asn	Leu	Leu	Gln 685	Asp	Pro	Asn
Phe	Arg 690	Gly	Ile	Asn	Arg	Gln 695	Leu	Asp	Arg	Gly	Trp 700	Arg	Gly	Ser	Thr
Asp 705	Ile	Thr	Ile	Gln	Gly 710	Gly	Asp	Asp	Val	Phe 715	Lys	Glu	Asn	Tyr	Val 720
Thr	Leu	Leu	Gly	Thr 725		Asp	Glu	Cys	Tyr 730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Lys	Ile	Asp	Glu 740	Ser	Lys	Leu	Lys	Ala 745	Tyr	Thr	Arg	Tyr	Gln 750	Leu	Arg

- Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 755 760 765
- Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 770 775 780
- Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 785 790 795 800
- Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815
- Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 820 825 830
- Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845
- Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 855 860
- Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880
- Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895
- Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910
- Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925
- Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 940
- Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960
- Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975
- Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990
- Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005
- Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020
- Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040
- Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050 1055
- Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Glu Glu Tyr Glu Gly Thr 1075 1080 1085	
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100	
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120	
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135	
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150	
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165	
Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180	
(2) INFORMATION FOR SEQ ID NO:12:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3546 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "Synthetic DNA"</pre>	
(iii) HYPOTHETICAL: NO	
<pre>(iii) HYPOTHETICAL: NO (ix) FEATURE:</pre>	
<pre>(ix) FEATURE:</pre>	
<pre>(ix) FEATURE:</pre>	48
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 13543 (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)" /note= "Disclosed in Figure 11 as contained in pCIB5512" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	4 8
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 13543 (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)" /note= "Disclosed in Figure 11 as contained in pCIB5512" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1185 1190 AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	

TGG GGC ATC TTC Trp Gly Ile Phe	GGC CCC AGC CAGC CAGC Pro Ser GI	AG TGG GAC GCC ln Trp Asp Ala 1255	TTC CTG GTG Phe Leu Val	CAG ATC 240 Gln Ile 1260
GAG CAG CTG ATC Glu Gln Leu Ile 126	Asn Gln Arg I	rc gag gag ttc le Glu Glu Phe 1270	GCC CGC AAC Ala Arg Asn 1275	Gln Ala
ATC AGC CGC CTG Ile Ser Arg Leu 1280	Glu Gly Leu Se	GC AAC CTG TAC er Asn Leu Tyr 285	CAA ATC TAC Gln Ile Tyr 1290	GCC GAG 336 Ala Glu
AGC TTC CGC GAG Ser Phe Arg Glu 1295	TGG GAG GCC GA Trp Glu Ala As 1300	AC CCC ACC AAC sp Pro Thr Asn	CCC GCC CTG Pro Ala Leu 1305	CGC GAG 384 Arg Glu
GAG ATG CGC ATC Glu Met Arg Ile 1310	CAG TTC AAC GA Gln Phe Asn As 1315	AC ATG AAC AGC sp Met Asn Ser 132	Ala Leu Thr	ACC GCC 432 Thr Ala 1325
ATC CCC CTG TTC Ile Pro Leu Phe	GCC GTG CAG AN Ala Val Gln An 1330	AC TAC CAG GTG sn Tyr Gln Val 1335	CCC CTG CTG Pro Leu Leu	AGC GTG 480 Ser Val 1340
TAC GTG CAG GCC Tyr Val Gln Ala 134	Ala Asn Leu H	AC CTG AGC GTG is Leu Ser Val 1350	CTG CGC GAC Leu Arg Asp 1355	Val Ser
GTG TTC GGC CAG Val Phe Gly Gln 1360	Arg Trp Gly Pl	TC GAC GCC GCC he Asp Ala Ala 365	ACC ATC AAC Thr Ile Asn 1370	AGC CGC 576 Ser Arg
TAC AAC GAC CTG Tyr Asn Asp Leu 1375	ACC CGC CTG A Thr Arg Leu I 1380	TC GGC AAC TAC le Gly Asn Tyr	ACC GAC CAC Thr Asp His 1385	GCC GTG 624 Ala Val
CGC TGG TAC AAC Arg Trp Tyr Asn 1390	ACC GGC CTG G Thr Gly Leu G 1395	AG CGC GTG TGG lu Arg Val Trp 140	Gly Pro Asp	AGC CGC 672 Ser Arg 1405
GAC TGG ATC AGG Asp Trp Ile Arg	TAC AAC CAG T Tyr Asn Gln P 1410	TC CGC CGC GAG he Arg Arg Glu 1415	CTG ACC CTG	ACC GTG 720 Thr Val 1420
CTG GAC ATC GTG Leu Asp Ile Val 142	. Ser Leu Phe P	CC AAC TAC GAC ro Asn Tyr Asp 1430	AGC CGC ACC Ser Arg Thr 1435	Tyr Pro
ATC CGC ACC GTG Ile Arg Thr Val 1440	Ser Gln Leu T	CC CGC GAG ATT hr Arg Glu Ile 445	TAC ACC AAC Tyr Thr Asn 1450	CCC GTG 816 Pro Val
CTG GAG AAC TTC Leu Glu Asn Phe 1455	GAC GGC AGC TASP Gly Ser P	TC CGC GGC AGC he Arg Gly Ser	GCC CAG GGC Ala Gln Gly 1465	ATC GAG 864 Ile Glu
GGC AGC ATC CGC Gly Ser Ile Arg 1470			e Leu Asn Ser	
ATC TAC ACC GAC	GCC CAC CGC G	GC GAG TAC TAC	TGG AGC GGC	CAC CAG 960

TIE TYL THE ASP	Ala His Arg 1490		yr Tyr Trp 9 495	Ser Gly His 150	
ATC ATG GCC AGC Ile Met Ala Ser 150	Pro Val Gly	TTC AGC G Phe Ser G 1510	GC CCC GAG 1	PTC ACC TTC Phe Thr Phe 1515	CCC 1008 Pro
CTG TAC GGC ACC Leu Tyr Gly Thr 1520			ro Gln Gln A		
CAG CTG GGC CAG Gln Leu Gly Gln 1535		Arg Thr L			
CGA CCT TTC AAC Arg Pro Phe Asn 1550					
GGC ACC GAG TTC Gly Thr Glu Phe	GCC TAC GGC Ala Tyr Gly 1570	y Thr Ser S	GC AAC CTG (Ser Asn Leu I .575	CCC AGC GCC Pro Ser Ala 158	Val
TAC CGC AAG AGC Tyr Arg Lys Ser 158	Gly Thr Va	G GAC AGC C l Asp Ser L 1590	TG GAC GAG A eu Asp Glu I	ATC CCC CCT Ile Pro Pro 1595	CAG 1248 Gln
AAC AAC AAC GTG Asn Asn Asn Val 1600			he Ser His A		
GTG AGC ATG TTC Val Ser Met Phe					
1615	16		1625	vai ser lie	IIe
	TTC AGC TG	20 G ATT CAC C	1625 CGC AGT GCC (GAG TTC AAC	AAC 1392
CGT GCA CCT ATG Arg Ala Pro Met 1630 ATC ATC CCC AGC Ile Ile Pro Ser	TTC AGC TGC Phe Ser Try 1635 AGC CAG ATC Ser Gln Ile	G ATT CAC C O Ile His A C ACC CAG A e Thr Gln I	1625 CGC AGT GCC (Arg Ser Ala (1640 ATC CCC CTG 2	GAG TTC AAC Glu Phe Asn ACC AAG AGC Thr Lys Ser	AAC 1392 Asn 1645 ACC 1440 Thr
CGT GCA CCT ATG Arg Ala Pro Met 1630 ATC ATC CCC AGC Ile Ile Pro Ser	TTC AGC TGPhe Ser Try 1635 AGC CAG ATCS Ser Gln Ill 1650 GGC ACC AGGly Thr Ser	G ATT CAC CO Ile His A C ACC CAG A E Thr Gln I 1 C GTG GTG A	GC AGT GCC (Arg Ser Ala (1640) ATC CCC CTG ATC Leu 1655	GAG TTC AAC Glu Phe Asn ACC AAG AGC Thr Lys Ser 166 GGC TTC ACC	AAC 1392 Asn 1645 ACC 1440 Thr 0
CGT GCA CCT ATG Arg Ala Pro Met 1630 ATC ATC CCC AGC Ile Ile Pro Ser AAC CTG GGC AGC Asn Leu Gly Ser	TTC AGC TGC Phe Ser Try 1635 AGC CAG ATC Ser Gln Ilc 1650 GGC ACC AGC Gly Thr Sec 5	G ATT CAC CO Ile His A C ACC CAG A e Thr Gln I C GTG GTG A r Val Val L 1670 C AGC CCC G	1625 CGC AGT GCC (Arg Ser Ala (1640) ATC CCC CTG ATC (ATC CCC CTG ATC	GAG TTC AAC Glu Phe Asn ACC AAG AGC Thr Lys Ser 166 GGC TTC ACC Gly Phe Thr 1675 AGC ACC CTG	AAC 1392 Asn 1645 ACC 1440 Thr 0 GGC 1488 Gly CGC 1536
CGT GCA CCT ATG Arg Ala Pro Met 1630 ATC ATC CCC AGC Ile Ile Pro Ser AAC CTG GGC AGC Asn Leu Gly Ser 166 GGC GAC ATC CTG Gly Asp Ile Leu	TTC AGC TGC Phe Ser Try 1635 AGC CAG ATC Ser Gln Ilc 1650 GGC ACC AGC Gly Thr Seconds CGC CGC ACC Arg Arg The	G ATT CAC CO Ile His A C ACC CAG A E Thr Gln I C GTG GTG A r Val Val L 1670 C AGC CCC G r Ser Pro G 1685 G AGC CAG C u Ser Gln A	1625 CGC AGT GCC (Arg Ser Ala (1640) ATC CCC CTG ATC (ATC CCC CTG ATC	GAG TTC AAC Glu Phe Asn ACC AAG AGC Thr Lys Ser 166 GGC TTC ACC Gly Phe Thr 1675 AGC ACC CTG Ser Thr Leu 1690 GTC CGC ATC	AAC 1392 Asn 1645 ACC 1440 Thr 0 GGC 1488 Gly CGC 1536 Arg
CGT GCA CCT ATG Arg Ala Pro Met 1630 ATC ATC CCC AGC Ile Ile Pro Ser AAC CTG GGC AGC Asn Leu Gly Ser 166 GGC GAC ATC CTG Gly Asp Ile Leu 1680 GTG AAC ATC ACC Val Asn Ile Thr	TTC AGC TGC Phe Ser Try 1635 AGC CAG ATC Ser Gln Ilc 1650 GGC ACC AGC Gly Thr Sec 5 CGC CGC ACC Arg Arg Th GCC CCC CT Ala Pro Lec 17 ACC AAC CT	G ATT CAC CO Ile His A C ACC CAG A E Thr Gln I C GTG GTG A r Val Val L 1670 C AGC CCC G r Ser Pro G 1685 G AGC CAG C u Ser Gln A 00 G CAG TTC C	AGC AGT GCC (Arg Ser Ala (1640) ATC CCC CTG ATC (ATC CCC CTG ATC	GAG TTC AAC Glu Phe Asn ACC AAG AGC Thr Lys Ser 166 GGC TTC ACC Gly Phe Thr 1675 AGC ACC CTG Ser Thr Leu 1690 GTC CGC ATC Val Arg Ile	AAC 1392 Asn 1645 ACC 1440 Thr 0 GGC 1488 Gly CGC 1536 Arg CGC 1584 Arg CGC 1632

1730 1735 1740

	CAG Gln			Ser					Gly					Phe		1728
	AGC Ser		Gly					Thr					Val			1776
AGC Ser	GGC Gly 1775	Asn	GAG Glu	GTG Val	TAC Tyr	ATC Ile 1780	Asp	CGC Arg	ATC Ile	GAG Glu	TTC Phe 1785	Val	CCC Pro	GCC Ala	GAG Glu	1824
	ACC Thr					Tyr					Ala					1872
	GAG Glu				Ser					Gly					Val	1920
ACC Thr	GAC Asp	TAC- Tyr	CAC His 1825	Ile	GAT Asp	CAG Gln	GTG Val	AGC Ser 1830	Asn	CTG Leu	GTG Val	GAG Glu	TGC Cys 1835	Leu	AGC Ser	1968
	GAG Glu		Cys					Lys					Lys			2016
CAC His	GCC Ala 185	Lys	CGC Arg	CTG Leu	AGC Ser	GAC Asp 1860	Glu	CGC Arg	AAC Asn	CTG Leu	CTG Leu 1865	Gln	GAC Asp	CCC Pro	AAC Asn	2064
	CGC Arg					Gln					Trp					2112
GA:	ATC Ile	ACC Thr	ATC Ile	CAG Gln 1890	Gly	GGC Gly	GAC Asp	GAC Asp	GTG Val 1895	Phe	AAG Lys	GAG Glu	AAC Asn	TAC Tyr 1900	Val	2160
	CTG Leu			Thr					Tyr					Tyr		2208
	G ATC		Glu					Ala					Gln			2256
GG(Gl	TAC Tyr 193	Ile	GAG Glu	GAC Asp	AGC Ser	CAG Gln 1940	Asp	CTG Leu	GAA Glu	ATC Ile	TAC Tyr 1945	Leu	ATC Ile	CGC Arg	TAC Tyr	2304
	C GCC n Ala 50					Val					Thr					2352
	C CTG Leu				Ser					Cys					Arg	2400

TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005 2010	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2041	
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 212	
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2200	
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	

GGA GAA GGT Gly Glu Gly	TGC GTA ACC Cys Val Thr 2225	Ile His G	GAG ATC Glu Ile 2230	GAG AAC A Glu Asn A	AT ACA GAC sn Thr Asp 2235	GAA 3168 Glu
CTG AAG TTT Leu Lys Phe 2240	Ser Asn Cys	GTA GAA G Val Glu G 2245	GAG GAA Glu Glu	Val Tyr P	CA AAC AAC ro Asn Asn 250	ACG 3216 Thr
GTA ACG TGT Val Thr Cys 2255	AAT GAT TAT Asn Asp Tyr	ACT GCG A Thr Ala T 2260	ACT CAA Thr Gln	GAA GAA T Glu Glu T 2265	AT GAG GGT Yr Glu Gly	ACG 3264 Thr
TAC ACT TCT Tyr Thr Ser 2270	CGT AAT CGA Arg Asn Arg 227	Gly Tyr A	Asp Gly	GCC TAT G Ala Tyr G 2280	AA AGC AAT lu Ser Asn	TCT 3312 Ser 2285
TCT GTA CCA Ser Val Pro	GCT GAT TAT Ala Asp Tyr 2290	GCA TCA G Ala Ser A	GCC TAT Ala Tyr 2295	Glu Glu L	AA GCA TAT ys Ala Tyr 230	Thr
GAT GGA CGA Asp Gly Arg	AGA GAC AAT Arg Asp Asn 2305	Pro Cys C	GAA TCT Glu Ser 2310	AAC AGA G Asn Arg G	GA TAT GGG ly Tyr Gly 2315	GAT 3408 Asp
TAC ACA CCA Tyr Thr Pro 2320	Leu Pro Ala	GGC TAT G Gly Tyr V 2325	GTG ACA Val Thr	Lys Glu L	TA GAG TAC eu Glu Tyr 330	TTC 3456 Phe
CCA GAA ACC Pro Glu Thr 2335	GAT AAG GTA Asp Lys Val	TGG ATT C Trp Ile C 2340	GAG ATC Glu Ile	GGA GAA A Gly Glu T 2345	CG GAA GGA hr Glu Gly	ACA 3504 Thr
TTC ATC GTG Phe Ile Val 2350	GAC AGC GTG Asp Ser Val 235	Glu Leu I	Leu Leu	ATG GAG G Met Glu G 2360	AA TAA lu	3546

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1181 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

65					70					13					00	
Glu	Gln	Leu	Ile	Asn 85	Gln	Arg	Ile	Glu	Glu 90	Phe	Ala	Arg	Asn	Gln 95	Ala	
Ile	Ser	Arg	Leu 100	Glu	Gly	Leu	Ser	Asn 105	Leu	Tyr	Gln	Ile	Tyr 110	Ala	Glu	
Ser	Phe	Arg 115	Glu	Trp	Glu	Ala	Asp 120	Pro	Thr	Asn	Pro	Ala 125	Leu	Arg	Glu	
Glu	Met 130	Arg	Ile	Gln	Phe	Asn 135	Asp	Met	Asn	Ser	Ala 140	Leu	Thr	Thr	Ala	
Ile 145	Pro	Leu	Phe	Ala	Val 150	Gln	Asn	Tyr	Gln	Val 155	Pro	Leu	Leu	Ser	Val 160	
Tyr	Val	Gln	Ala	Ala 165	Asn	Leu	His	Leu	Ser 170	Val	Leu	Arg	Asp	Val 175	Ser	
Val	Phe	Gly	Gln 180	Arg	Trp	Gly	Phe	Asp 185	Ala	Ala	Thr	Ile	Asn 190	Ser	Arg	
Tyr	Asn	Asp 195	Leu	Thr	Arg	Leu	Ile 200	Gly	Asn	Tyr	Thr	Asp 205	His	Ala	Val	
Arg	Trp 210	Tyr	Asn	Thr	Gly	Leu 215	Glu	Arg	Val	Trp	Gly 220	Pro ,		Ser	Arg	
Asp 225		Ile	Arg	Tyr	Asn 230	Gln	Phe	Arg	Arg	Glu 235	Leu	Thr	Leu	Thr	Val 240	
Leu	Asp	Ile	Val	Ser 245	Leu	Phe	Pro	Asn	Tyr 250	Asp	Ser	Arg	Thr	Туг 255	Pro	
Ile	Arg	Thr	Val 260	Ser	Gln	Leu	Thr	Arg 265	Glu	Ile	Tyr	Thr	Asn 270	Pro	Val	
Leu	Glu	Asn 275		Asp	Gly	Ser	Phe 280	Arg	Gly	Ser	Ala	Gln 285	Gly	Ile	Glu	
Gly	Ser 290		Arg	Ser						Ile			Ser	Ile	Thr	
Ile 305		Thr	Asp	Ala	His 310	Arg	Gly	Glu	Tyr	Туг 315	Trp	Ser	Gly	His	Gln 320	
Ile	Met	Ala	Ser	Pro 325		Gly	Phe	Ser	Gly 330		Glu	Phe	Thr	Phe 335	Pro	
Leu	Tyr	Gly	Thr 340		Gly	Asn	Ala	Ala 345		Gln	Gln	. Arg	350	Val	Ala	
Gln	Leu	Gly 355		Gly	Val	Tyr	Arg 360		Leu	. Ser	Ser	Thr 365	Leu	Tyr	Arg	
Arg	370		a Asn	Ile	: Gly	11∈ 375		Asn	Gln	Gln	Leu 380	Ser	· Val	Leu	Asp	
Gly 385		Glu	ı Phe	e Ala	Туг 390		Thr	Ser	Ser	395	Leu	Pro	Ser	Ala	Val 400	

- Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
 405 410 415
- Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430
- Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 435 440 445
- Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 450 460
- Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 465 470 475 480
- Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
 485 490 495
- Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
 500 505 510
- Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 515 520 525
- Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 530 540
- Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 545 550 560
- Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 565 570 575
- Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 580 585 590
- Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 595 600
- Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 610 615 620
- Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 625 630 635 640
- Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 645 650 655
- Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 660 670
- His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 675 680 685
- Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 690 695 700
- Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 705 710 715 720

- Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 725 730 735
- Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 740 745 750
- Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
- Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
 770 780
- Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 785 790 795 800
- Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815
- Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 820 825 830
- Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845
- Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 860
- Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880
- Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895
- Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910
- Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925
- Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940
- Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960
- Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975
- Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990
- Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005
- Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020
- Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040
- Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu

T.eu	Tivs	Phe	Ser	Asn	Cvs	Val	Glu	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr
	-, -		1060		-4-			1069					1070)	

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 1170 1175 1180

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
 - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)" /note= "Disclosed in Figure 13 as contained in pCIB5513."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	GAC	AAC	AAC	CCC	AAC	ATC	AAC	GAG	TGC	ATC	CCC	TAC	AAC	TGC	CTG	48
Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	
	-		1189					1190					1195	5		

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

1200 1205 1210

TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser

1215 1220 1225

	Phe					Gly					Leu			ATC Ile		3	192
					Pro					Ala				CAG Gln 1260	Ile	2	240
				Asn					Glu					CAG Gln		2	288
			Leu					Asn					Tyr	GCC Ala		3	336
		Arg					Asp					Ala		CGC Arg		3	384
	Met					Asn					Ala			ACC Thr		4	132
					Val					Val				AGC Ser 1340	Val	4	180
				Ala					Ser					GTC Val		5	528
			Gln					Asp					Asn	AGC Ser		5	576
		Asp					Ile					Asp		GCC Ala		€	524
	Trp		Asn		Gly	Leu			Val		Gly			AGC Ser		6	572
					Asn					Glu				ACC Thr 1420	Val	7	720
				Ser					Tyr					TAC Tyr		7	768
_			Val					Arg					Asn	CCC Pro		8	316
		Asn					Phe					Gln		ATC Ile		8	364

GGC A Gly S 1470	AGC Ser	ATC Ile	CGC Arg	AGC Ser	CCC Pro 1475	His	CTG Leu	ATG Met	GAC Asp	ATC Ile 1480	Leu	AAC Asn	AGC Ser	ATC Ile	ACC Thr 1485		912
ATC 1	rac Cyr	ACC Thr	GAC Asp	GCC Ala 1490	His	CGC Arg	GGC Gly	GAG Glu	TAC Tyr 1495	Tyr	TGG Trp	AGC Ser	GGC Gly	CAC His 1500	GIN		960
ATC A	ATG Met	GCC Ala	AGC Ser 1505	Pro	GTC Val	GGC Gly	TTC Phe	AGC Ser 1510	Gly	CCC Pro	GAG Glu	TTC Phe	ACC Thr 1515	Phe	CCC Pro	1	L008
CTG :	TAC Tyr	GGC Gly 1520	Thr	ATG Met	GGC Gly	AAC Asn	GCT Ala 1525	Ala	CCT Pro	CAG Gln	CAG Gln	CGC Arg 1530	TTE	GTG Val	GCA Ala	3	1056
CAG (Gln)	CTG Leu 1535	Gly	CAG Gln	GGA Gly	GTG Val	TAC Tyr 1540	Arg	ACC Thr	CTG Leu	AGC Ser	AGC Ser 1545	Thr	CTG Leu	TAC Tyr	CGT Arg	:	1104
CGA (Arg 1	Pro	TTC Phe	AAC Asn	ATC Ile	GGC Gly 1555	Ile	AAC Asn	AAC Asn	CAG Gln	CAG Gln 1560	Leu	AGC Ser	GTG Val	CTG Leu	GAC Asp 1565	:	1152
GGC ;	ACC Thr	GAG Glu	TTC Phe	GCC Ala 157	Tyr	GGC Gly	ACC Thr	AGC Ser	AGC Ser 157	Asn	CTG Leu	CCC Pro	AGC Ser	GCC Ala 1580	vaı	:	1200
TAC	CGC Arg	AAG Lys	AGC Ser 158	Gly	ACC Thr	GTG Val	GAC Asp	AGC Ser 159	Leu	GAC Asp	GAG Glu	ATC Ile	CCC Pro 159	Pro	CAG Gln		1248
AAC Asn	AAC Asn	AAC Asn 160	Val	CCA Pro	CCT Pro	CGA Arg	CAG Gln 160	_Gly	TTC Phe	AGC Ser	CAC His	CGT Arg 161	Leu	AGC Ser	CAC His		1296
Val	AGC Ser 161	Met	TTC Phe	CGC Arg	AGT Ser	GGC Gly 162	Phe	AGC Ser	AAC Asn	AGC Ser	AGC Ser 162	Val	AGC Ser	ATC Ile	ATC Ile		1344
CGT Arg 1630	Ala	CCT Pro	ATG Met	TTC Phe	AGC Ser 163	Trp	ATT	CAC His	CGC Arg	AGT Ser 164	Ala	GAG Glu	TTC Phe	AAC Asn	AAC Asn 1645		1392
ATC Ile	ATC Ile	CCC Pro	AGC Ser	AGC Ser 165	CAG Gln	ATC Ile	ACC Thr	CAG Gln	ATC Ile 165	Pro	CTG Leu	ACC Thr	AAG Lys	AGC Ser 166	Thr		1440
AAC Asn	CTG Leu	GGC Gly	AGC Ser 166	: Gly	ACC Thr	AGC Ser	GTG Val	GTG Val 167	. Lys	GGC Gly	CCC Pro	GGC Gly	TTC Phe 167	Thr	GGC Gly		1488
GGC Gly	GAC Asp	ATC Ile	e Let	G CGC	C CGC J Arg	ACC Thr	AGC Ser 168	: Pro	: GGC : Gly	CAG Gln	ATC	AGC Ser 169	Thr	CTG Leu	CGC Arg		1536
GTG Val	AAC Asn 169	Ile	C ACC	C GCC	C CCC	CTG Lev 170	ı Ser	C CAC	G CGC	TAC TYI	CGC Arg	, Val	CGC Arg	ATC	CGC		1584
TAC	GCC	AGC	C ACC	C ACC	C AAC	CTC	CAC	G TTC	CAC	C ACC	: AGC	ATC	GAC	GGC	CGC		1632

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1710 1715 1720 1725	
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1730 1735 1740	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1745 1750 1755	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 1760 1765 1770	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1775 1780 1785	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1790 1795 1800 1805	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1810 1815 1820	1920
ACC GAC TAC CAC ATC GAC CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1825 1830 1835	1968
GAC GAG TTC TGC CTG GAC GAG AAG AAG GAG CTG AGC GAG AAG GTG AAG Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1840 1845 1850	2016
CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1855 1860 1865	2064
TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 1870 1875 1880 1885	2112
GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1890 1895 1900	2160
ACC CTG CAG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG Thr Leu Gln Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1905 1910 1915	2208
CCG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC Pro Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1920 1925 1930	2256
GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 1935 1940 1945	2304
AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp	2352

1950	1955	1960	1965
	Ser Pro Ile Gly	AAG TGC GGG GAG CCG A Lys Cys Gly Glu Pro A 1975 1	
		GAC CTA GAC TGC AGC T Asp Leu Asp Cys Ser C 1995	
		CAC CAC TTC AGC CTG G His His Phe Ser Leu A 2010	
		GAC CTG GGC GTG TGG G Asp Leu Gly Val Trp V 2025	
TTC AAG ATC AAG ACC Phe Lys Ile Lys Thr 2030	CAG GAC GGC CAC Gln Asp Gly His 2035	GCC CGC CTG GGC AAT C Ala Arg Leu Gly Asn L 2040	TA GAG 2592 eu Glu 2045
	Pro Leu Val Gly	GAG GCC CTG GCC CGC G Glu Ala Leu Ala Arg V 2055 2	
		CGC GAG AAG CTG GAG T Arg Glu Lys Leu Glu T 2075	
		GAG AGC GTG GAC GCC C Glu Ser Val Asp Ala L 2090	
		GCC GAC ACC AAC ATC G Ala Asp Thr Asn Ile A 2105	
		AGC ATT CGC GAG GCC T Ser Ile Arg Glu Ala T 2120	
CCC GAG CTG AGC GTG Pro Glu Leu Ser Val 2130	Ile Pro Gly Val	AAC GCC GCC ATC TTC G Asn Ala Ala Ile Phe G 2135	AG GAA 2880 lu Glu 140
		AGC CTG TAC GAC GCC C Ser Leu Tyr Asp Ala A 2155	
		GGC CTG AGC TGC TGG A Gly Leu Ser Cys Trp A 2170	
		AAC AAC CAC CGC AGC G Asn Asn His Arg Ser V 2185	
		AGC CAG GAG GTG CGC G Ser Gln Glu Val Arg V 2200	

CCC GGC CGC G Pro Gly Arg G					3120
GGC GAG GGC T Gly Glu Gly C		ı Ile Glu		Asp Glu	3168
CTC AAG TTC A Leu Lys Phe S 2240					3216
GTG ACC TGC A Val Thr Cys A 2255					3264
TAC ACC TCT C Tyr Thr Ser A 2270	Gly Tyr Asp		Tyr Glu Ser		3312
TCC GTG CCA G Ser Val Pro A					3360
GAC GGT AGA C Asp Gly Arg A		Ser Asn		Gly Asp	3408
TAC ACC CCC C Tyr Thr Pro I 2320					3456
CCC GAG ACC G Pro Glu Thr A 2335					3504
TTC ATC GTG 6 Phe Ile Val A 2350	 Glu Leu Leu		Glu Glu		3546

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1181 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

- Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
- Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
- Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
- Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110
- Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
- Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135
- Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
- Tyr Val Glm Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175
- Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
- Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205
- Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220
- Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240
- Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255
- Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270
- Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285
- Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300
- Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315 320
- Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335
- Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345
- Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 375 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 590 585 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 630 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 645 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 680

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr

690	695	700

Asp 705	Ile	Thr	Ile	Gln	Gly 710	Gly	Asp	Asp	Val	Phe 715	Lys	Glu	Asn	Tyr	Val 720
Thr	Leu	Gln	Gly	Thr 725	Phe	Asp	Glu	Cys	Tyr 730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Pro	Ile	qaA	Glu 740	Ser	Lys	Leu	Lys	Ala 745	Tyr	Thr	Arg	Tyr	Gln 750	Leu	Arg
Gly	Tyr	Ile 755	Glu	Asp	Ser	Gln	Asp 760	Leu	Glu	Ile	Tyr	Leu 765	Ile	Arg	Tyr
Asn	Ala 770	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro 785	Leu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Gly	Glu	Pro	Asn	Arg 800
Cys	Ala	Pro	His	Leu 805	Glu	Trp	Asn	Pro	Asp 810	Leu	Asp	Cys	Ser	Cys 815	Arg
Asp	Gly	Glu	Lys 820	Cys	Ala	His	His	Ser 825	His	His	Phe	Ser	Leu 830	Asp	Ile
Asp	Val	Gly 835	Cys	Thr	Asp	Leu	Asn 840	Glu	Asp	Leu	Gly	Val 845	Trp	Val	Ile
Phe	Lys 850	Ile	Lys	Thr	Gln	Asp 855	Gly	His	Ala	Arg	Leu 860	Gly	Asn	Leu	Glu
Phe 865	Leu	Glu	Glu	Lys	Pro 870	Leu	Val	Gly	Glu	Ala 875	Leu	Ala	Arg	Val	Lys 880
Arg	Ala	Glu	Lys	Lys 885	Trp	Arg	Asp	Lys	Arg 890	Glu	Lys	Leu	Glu	Trp 895	Glu
Thr	Asn	Ile	Val 900	Tyr	Lys	Glu	Ala	Lys 905	Glu	Ser	Val	Asp	Ala 910	Leu	Phe
Val	Asn	Ser 915	Gln	Tyr	Asp	Arg	Leu 920	Gln	Ala	Asp	Thr	Asn 925	Ile	Ala	Met
Ile	His 930	Ala	Ala	Asp	Lys	Arg 935	Val	His	Ser	Ile	Arg 940	Glu	Ala	Tyr	Leu
Pro 945	Glu	Leu	Ser	Val	Ile 950	Pro	Gly	Val	Asn	Ala 955	Ala	Ile	Phe	Glu	Glu 960
Leu	Glu	Gly	Arg	Ile 965	Phe	Thr	Ala	Phe	Ser 970	Leu	Tyr	Asp	Ala	Arg 975	Asn
Val	Ile	Lys	Asn 980	Gly	Asp	Phe	Asn	Asn 985	Gly	Leu	Ser	Cys	Trp 990	Asn	Val
Lys	Gly	His 995	Val	Asp	Val	Glu	Glu 100		Asn	Asn	His	Arg 1005	_	Val	Leu
Val	Val		Glu	Trp	Glu	Ala		Val	Ser	Gln	Glu 1020		Arg	Val	Cys

Pro Gly Arg Gly 7	Tyr Ile Leu Arg	Val Thr Ala Tyr	Lys Glu Gly Tyr
	1030	1035	1040
Gly Glu Gly Cys V	Val Thr Ile His	Glu Ile Glu Asn	Asn Thr Asp Glu
	1045	1050	1055
Leu Lys Phe Ser 2	Asn Cys Val Glu	ı Glu Glu Val Tyr 1065	Pro Asn Asn Thr 1070
Val Thr Cys Asn 7	Asp Tyr Thr Ala	a Thr Gln Glu Glu 30	Tyr Glu Gly Thr 1085
Tyr Thr Ser Arg 2	Asn Arg Gly Tyr	Asp Gly Ala Tyr	Glu Ser Asn Ser
	1095	110	O
Ser Val Pro Ala 2	Asp Tyr Ala Sei	r Ala Tyr Glu Glu	Lys Ala Tyr Thr
1105	1110	1115	1120
	Asp Asn Pro Cys	s Glu Ser Asn Arg	Gly Tyr Gly Asp
	1125	1130	1135
Tyr Thr Pro Leu		r Val Thr Lys Glu	Leu Glu Tyr Phe
1140		1145	1150
Pro Glu Thr Asp	Lys Val Trp Ile	e Glu Ile Gly Glu	Thr Glu Gly Thr
1155	11	60	1165
Phe Ile Val Asp	Ser Val Glu Le	u Leu Leu Met Glu	Glu
1170	1175	118	O
(2) INFORMATION	FOR SEQ ID NO:	16:	
(A) LE (B) TY (C) ST	E CHARACTERIST NGTH: 3547 bas PE: nucleic ac RANDEDNESS: si POLOGY: linear	e pairs id ngle	
(ii) MOLECUI	E TYPE: other :	nucleic acid	NA"
(A) DE	ESCRIPTION: /de	sc = "Synthetic I	
(iii) HYPOTHE	ETICAL: NO		
(B) L((D) OT	AME/KEY: CDS CCATION: 1354 THER INFORMATIO	N: /product= "Ful	l-length, hybrid,
	CE DESCRIPTION:		

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

ATG GAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

1185

1190

1195

48

96

1200 1205 1210

TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215 1220 1225	144
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG G	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu ThroThr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816

CTG GAG AAC Leu Glu Asn 1455					
GGC AGC ATC Gly Ser Ile 1470		His Leu 1	Met Asp I		
ATC TAC ACC					Gln
ATC ATG GCC . Ile Met Ala		Gly Phe S			
CTG TAC GGC : Leu Tyr Gly '	Thr Met Gly			Ile Val	
CAG CTG GGC GIn Leu Gly 1535					
CGA CCT TTC Arg Pro Phe 1		Ile Asn A	Asn Gln G		
GGC ACC GAG					Val
TAC CGC AAG . Tyr Arg Lys		Val Asp S			
AAC	Val Pro Pro			Leu Ser	
GTG AGC ATG ' Val Ser Met : 1615					
CGT GCA CCT Arg Ala Pro 1		Trp Ile H	His Arg Se		
ATC ATC CCC I					Thr
AAC CTG GGC A		Ser Val V			
GGC GAC ATC (Gly Asp Ile 1 1680	Leu Arg Arg			Thr Leu	

GTG Val	AAC Asn 1695	Ile	ACC Thr	GCC Ala	CCC Pro	CTG Leu 1700	Ser	CAG Gln	CGC Arg	TAC Tyr	CGC Arg 1705	Val	CGC Arg	ATC Ile	CGC Arg	158≟
	Ala					Leu				ACC Thr 1720	Ser					1632
					Asn					ATG Met					Asn	1680
CTG Leu	CAG Gln	AGC Ser	GGC Gly 1745	Ser	TTC Phe	CGC Arg	ACC Thr	GTG Val 1750	Gly	TTC Phe	ACC Thr	ACC Thr	CCC Pro 1755	Phe	AAC Asn	1728
			Gly					Thr		AGC Ser			Val			1776
AGC Ser	GGC Gly 1775	Asn	GAG Glu	GTG Val	TAC Tyr	ATC Ile 1780	Asp	CGC Arg	ATC Ile	GAG Glu	TTC Phe 1785	Val	CCC Pro	GCC Ala	GAG Glu	1824
GTG Val 1790	Thr	TTC Phe	GAG Glu	GCC Ala	GAG Glu 1795	Tyr	GAC Asp	CTG Leu	GAG Glu	AGG Arg 1800	Ala	CAG Gln	AAG Lys	GCC Ala	GTG Val 1805	1872
					Ser					GGC Gly					Val	1920
ACC Thr	GAC Asp	TAC Tyr	CAC His 1825	Ile	GAT Asp	CAA Gln	GTA Val	TCC Ser 1830	Asn	TTA Leu	GTT Val	GAG Glu	TGT Cys 1835	Leu	TCT Ser	1968
GAT Asp	GAA Glu	TTT Phe 1840	Суѕ	CTG Leu	GAT Asp	GAA Glu	AAA Lys 1845	Lys	GAA Glu	TTG Leu	TCC Ser	GAG Glu 1850	Lys	GTC Val	AAA Lys	2016
		Lys					Glu			TTA Leu		Gln				2064
TTT Phe 1870	Arg	GGG Gly	ATC Ile	AAT Asn	AGA Arg 1875	Gln	CTA Leu	GAC Asp	CGT Arg	GGC Gly 1880	Trp	AGA Arg	GGA Gly	AGT Ser	ACG Thr 1885	2112
GAT Asp	ATT Ile	ACC Thr	ATC Ile	CAA Gln 1890	Gly	GGC Gly	GAT Asp	GAC Asp	GTA Val 1895	TTC Phe	AAA Lys	GAG Glu	AAT Asn	TAC Tyr 1900	Val	2160
				Thr					Tyr	CCA Pro				Tyr		2208
AAA Lys	ATA Ile	GAT Asp 1920	Glu	TCG Ser	AAA Lys	TTA Leu	AAA Lys 1925	Ala	TAT Tyr	ACC Thr	CGT Arg	TAC Tyr 1930	Gln	TTA Leu	AGA Arg	2256
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304

Gly	Tyr 1935		Glu	Asp	Ser	Gln 1940	Asp)	Leu	Glu	Ile	Tyr 1945	_	Ile	Arg	Tyr	
	Ala					Val	AAT Asn				Thr					2352
					Ser		ATC Ile			Cys					Arg	2400
				Leu			AAC Asn		Asp					Cys		2448
			Lys				CAC His 2005	Ser					Leu			2496
		Gly					AAC Asn					Val				2544
	Lys					Asp	GGC Gly				Leu					2592
					Pro		GTA Val			Ala					Lys	2640
				Lys			GAC Asp		Arg					Trp		2688
			Val				GCA Ala 2085	Lys					Ala			2736
		Ser					TTA Leu)					Asn				2784
	His					Arg	GTT Val				Arg					2832
					Ile		GGT Gly			Ala					Glu	2880
				Ile			GCA Ala		Ser					Arg		2928
			Asn				AAT Asn 2165	Asn					Trp			2976
							GAA Glu									3024

2175 2180 2185

A TGG GAA GCA GAA u Trp Glu Ala Glu 2195		Glu Val Arg V	
C TAT ATC CTT CGT y Tyr Ile Leu Arg 2210		Tyr Lys Glu (
C GTA ACC ATT CAT s Val Thr Ile His 25			
C AAC TGT GTA GAA r Asn Cys Val Glu 224	. Glu Glu Val		
I GAT TAT ACT GCG n Asp Tyr Thr Ala 2260			
I AAT CGA GGA TAT g Asn Arg Gly Tyr 2275		Tyr Glu Ser A	
r GAT TAT GCA TCA a Asp Tyr Ala Ser 2290		Glu Lys Ala	
A GAC AAT CCT TGT g Asp Asn Pro Cys 05			
A CCA GCT GGC TAT u Pro Ala Gly Tyr 232	Val Thr Lys		
I AAG GTA TGG ATT p Lys Val Trp Ile 2340			
C AGC GTG GAA TTA p Ser Val Glu Leu 2355		Glu Glu	3547

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1181 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

- Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30
- Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
- Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
- Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile .65 70 75 80
- Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
- Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110
- Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125
- Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140
- Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160
- Tyr Val Gln Ala Asa Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175
- Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
- Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205
- Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220
- Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240
- Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255
- Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270
- Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285
- Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300
- Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315 320
- Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335
- Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 360 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 520 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 535 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 570 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 595 600 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 625 635 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 665

- His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 675 680 685
- Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 690 695 700
- Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 705 710 715 720
- Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 725 730 735
- Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
 740 745 750
- Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 755 760 765
- Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 770 780
- Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 785 790 795 800
- Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815
- Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 820 825 830
- Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845
- Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 855 860
- Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880
- Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895
- Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910
- Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925
- Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940
- Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960
- Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975
- Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990

- Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005
- Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020
- Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040
- Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050 1055
- Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060 1065 1070
- Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075 1080 1085
- Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100
- Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120
- Asp Gly Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135
- Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150
- Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165
- Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180
- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794 ..2871, 3001..3135, 3236..3370)
 - (D) OTHER INFORMATION: /product= "maize TrpA" /note= "Maize TrpA sequence as disclosed in Figure 24."
 - (ix) FEATURE:
 - (A) NAME/KEY: TATA_signal
 (B) LOCATION: 1594..1599
 - (ix) FEATURE:

- (A) NAME/KEY: CAAT_signal(B) LOCATION: 1495..1499
- (ix) FEATURE:
 - (A) NAME/KEY: promoter (B) LOCATION: 39..1838
- (D) OTHER INFORMATION: /function= "Promoter sequence used in pCIB4433"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

			~		2011101 2101	(711) 01
60	TAATGAGCTC	AGATCTAGTT	CAGATTCTAG	AGTCTTTGAA	CCATTAAAGA	GAATTCGGAT
120	GTTATGTTTT	CAGGGGTACT	GCCATTAGGG	CAGCGGGGAG	TGAAAAAATT	CCAAAAGTCT
180	AAGGATCCTG	GTTTTGTAAG	AAAGAGAAAT	GATCTCTTCT	CCACTTTCTT	AAAGAGAACA
240	GGCAAGAGAG	AGATATTAGA	TTTTTCATAG	CATCGGCAAA	CCAACCTTTT	TCCTCCTCAT
300	CTCATCTTCA	TGATACCTCC	GCCACCTGGT	AATGGAAGTG	GATCCATGTA	GGGCCAAAAA
360	TTCCCTTTTG	CTTCTTTTTC	ATTTTAAACT	AAGTGAATGG	CATTATGAAA	ACAGAAAATC
420	CTGTCCCTAG	ATTAATGAAT	CATCACCCTC	GTATTATTCT	AAAATATCTG	CAATGAGCTG
480	CACTCCATAT	TCTTAAATTC	CCACCATGTT	CCTTCTGCAG	TCTCTTGATC	CAATTTGCTT
540	TTCTCAAGGA	CTCTCTCATT	TGGCTGCAAT	GAATCTGAGA	CAATCTATCA	CAAGCTTTTC
600	ACATTTATAT	TTTCCCTTCG	ACTTCTTATA	TATTTCTTGA	ATCCATAAGG	TATCGATGTT
660	CAAACATCGA	TTTTCCTTTC	TTTTTTGTTT	TTGTTCAATC	CAACATTTTT	TCCATCCTTT
720	CTTTAAAGTC	AAACCTTCTG	AGCTTTCAAA	GGTAAGGACG	GCTCCTCACA	TACATTTCCT
780	TGGGACAGAG	TCTTCTTAGT	CTAAAGTCCC	GCTCACATAT	CTCCAGCAAA	AGGTCTGAGC
840	GCCCAGAGAC	ATCATATTTA	GAAAAAAAAA	AACATGACCA	GACACATGGG	TCAGTGCTAA
900	CCCAACTTCT	AAGGAATCTA	TGGGCTAGCA	AGTCTCGTTA	TTGTACTGCA	AACAATATTC
960	ATCAAACTGT	TTCCAACTCT	TATTCATCAG	GTATATAGAC	GGGATGTCAA	CAAATGTGTT
1020	CTCATATTTG	TGTTCTTATC	TCCATCTATT	AATAAAGTGC	TATAGAGTTG	GCAGCTCAAT
1080	AGTGGCTCGC	CACCATTTAA	ATTTAAAGTG	TCCCACCAAC	TAAAATCACC	GTTAAGATAT
1140	CCCTTTTCTA	GGCAGCGGGA	TTAGCACGTT	CCGGAAATGT	CCGCTGAAAA	GAGCACCAAA
1200	CATCCTGTAG	AACGCTCCTC	CCCACGGGCC	TCCACCACGG	TTCTTCGTTG	TCTCATCGTG
				: CGACCGAGCC		
1320	CACATGGGAT	GAGATTCACT	TACGTGAGGT	CTACGTATAC	TGTGGCACTC	CAGCCAGCCA
1380	TATGACGATT	. ATAAAGCATT	GTGAGAGATA	CTGTGGTTGT	TATTTTACTO	GGGACCGAGA
				G CGTCCAGATA		
				A TATATATATA		

TATAATTCAT TTGACTTTTT TATCCACCGA TGCTCGTTTT ATTAAAAAAA ATATTATAAT	1560
TATTGTTACT TTTTGTTGTA ATATTGTTTA GCATATAATA AACTTTGATA CTAGTATGTT	1620
TCCGAGCAAA AAAAAATATT AATATTTAGA TTACGAGCCC ATTAATTAAT TATATTCGAG	1688
ACAAGCGAAG CAAAGCAAAG CAAGCTAATG TTGCCCCTGC TGTGCATGCA GAGGCCCGCT	1740
CTTGCTATAA ACGAGGCAGC TAGACGCGAC TCGACTCATC AGCCTCATCA ACCTCGACGA	1809
AGGAGGAACG AACGGACAGG TTGTTGCACA GAAGCGAC ATG GCT TTC GCG CCC Met Ala Phe Ala Pro 1 5	1853
AAA ACG TCC TCC TCC TCG CTG TCC TCG GCG TTG CAG GCA GCT CAG Lys Thr Ser Ser Ser Ser Leu Ser Ser Ala Leu Gln Ala Ala Gln 10 15 20	1901
TCG CCG CCG CTG CTC CTG AGG CGG ATG TCG TCG ACC GCA ACA CCG AGA Ser Pro Pro Leu Leu Arg Arg Met Ser Ser Thr Ala Thr Pro Arg 25 30 35	1949
CGG AGG TAC GAC GCG GCC GTC GTC GTC ACT ACC ACC ACT GCT AGA Arg Arg Tyr Asp Ala Ala Val Val Thr Thr Thr Thr Thr Ala Arg 40 45 50	1997
GCT GCG GCG GCT GCT GTC ACG GTT CCC GCC GCC CCG CCG CAG GCC Ala Ala Ala Ala Val Thr Val Pro Ala Ala Pro Pro Gln Ala Gly 55 60 65	2045
CGC CGC CGC CGG TGC CAC CAA AGC AAG CGG CGG CAC CCG CAG AGG AG	2093
AGC CGT CCG GTG TCG GAC ACC ATG GCG GCG CTC ATG GCC AAG GGC AAG Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu Met Ala Lys Gly Lys 90 95 100	2141
GTTCGTATAG TACGCGCGCG TGTCGTCGTC GTTATTTTGC GCATAGGCGC GGACATACAC	2201
GTGCTTTAGC TAGCTAACAG CTAGATCATC GGTGCAG ACG GCG TTC ATC CCG TAC Thr Ala Phe Ile Pro Tyr 105	2256
ATC ACC GCC GGC GAC CCG GAC CTA GCG ACG ACG GCC GAG GCG CTG CGT Ile Thr Ala Gly Asp Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg 110 120	2304
CTG CTG GAC GGC TGT GGC GCC GAC GTC ATC GAG CTG GGG GTA CCC TGC Leu Leu Asp Gly Cys Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys 125 130 135	2352
TCG GAC CCC TAC ATC GAC GGG CCC ATC ATC CAG GCG TCG GTG GCG CGG Ser Asp Pro Tyr Ile Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg 140 145 150 155	2400
GCT CTG GCC AGC GGC ACC ACC ATG GAC GCC GTG CTG GAG ATG CTG AGG Ala Leu Ala Ser Gly Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg 160 165 170	2448

GAG GTG ACG CCG GAG CTG TCG TGC CCC GTG GTG CTC CTC TAC TAC Glu Val Thr Pro Glu Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr 175 180 185	2496
AAG CCC ATC ATG TCT CGC AGC TTG GCC GAG ATG AAA GAG GCG GGG GTC Lys Pro Ile Met Ser Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val 190 200	2544
CAC GGTAACTATA GCTAGCTCTT CCGATCCCCC TTCAATTAAT TAATTTATAG His	2597
TAGTCCATTC ATGTGATGAT TTTTGTTTTT CTTTTTACTG ACA GGT CTT ATA GTG Gly Leu Ile Val 205	2652
CCT GAT CTC CCG TAC GTG GCC GCG CAC TCG CTG TGG AGT GAA GCC AAG Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 220	2700
AAC AAC AAC CTG GAG CTG GTAGGTTGAA TTAAGTTGAT GCATGTGATG Asn Asn Asn Leu Glu Leu 225 230	2748
ATTTATGTAG CTAGATCGAG CTAGCTATAA TTAGGAGCAT ATCAG GTG CTG Val Leu Leu	2802
ACA ACA CCA GCC ATA CCA GAA GAC AGG ATG AAG GAG ATC ACC AAG GCT Thr Thr Pro Ala Ile Pro Glu Asp Arg Met Lys Glu Ile Thr Lys Ala 235 240 245	2850
TCA GAA GGC TTC GTC TAC CTG GTAGTTATAT GTATATATAG ATGGACGACG Ser Glu Gly Phe Val Tyr Leu 250 255	2901
TAACTCATTC CAGCCCCATG CATATATGGA GGCTTCAATT CTGCAGAGAC GACGAAGACC	2961
ACGACGACGA CTAACACTAG CTAGGGGCGT ACGTTGCAG GTG AGC GTG AAC GGA Val Ser Val Asn Gly 260	3015
GTG ACA GGT CCT CGC GCA AAC GTG AAC CCA CGA GTG GAG TCA CTC ATC Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg Val Glu Ser Leu Ile 265 270 275	3063
CAG GAG GTT AAG AAG GTG ACT AAC AAG CCC GTT GCT GTT GGC TTC GGC Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val Ala Val Gly Phe Gly 280 285	3111
ATA TCC AAG CCC GAG CAC GTG AAG CAGGTACGTA CGTAGCTGAC CAAAAAAAAC Ile Ser Lys Pro Glu His Val Lys 295 300	3165
TGTTAACAAG TTTTGTTTGA CAAGCCGGCT ACTAGCTAGC TAACAGTGAT CAGTGACACA	3225
CACACACACA CAG ATT GCG CAG TGG GGC GCT GAC GGG GTG ATC ATC GGC Gln Ile Ala Gln Trp Gly Ala Asp Gly Val Ile Ile Gly 305	3274
AGC GCC ATG GTG AGG CAG CTG GGC GAA GCG GCT TCT CCC AAG CAA GGC	3322

Ser Ala Met Val Arg Gln Leu Gly Glu Ala Al 315 320 32	a Ser Pro Lys Gln Gly 5 330
CTG AGG AGG CTG GAG GAG TAT GCC AGG GGC AT Leu Arg Arg Leu Glu Glu Tyr Ala Arg Gly Me 335	G AAG AAC GCG CTG CCA 3370 et Lys Asn Ala Leu Pro 345
TGAGTCCATG ACAAAGTAAA ACGTACAGAG ACACTTGAT	A ATATCTATCT ATCATCTCGG 3430
AGAAGACGAC CGACCAATAA AAATAAGCCA AGTGGAAGT	G AAGCTTAGCT GTATATACAC 3490
CGTACGTCGT CGTCGTCGTT CCGGATCGAT CTCGGCCGG	C TAGCTAGCAG AACGTGTACG 3550
TAGTAGTATG TAATGCATGG AGTGTGGAGC TACTAGCTA	AG CTGGCCGTTC ATTCGATTAT 3610
AATTCTTCGC TCTGCTGTGG TAGCAGATGT ACCTAGTCG	A TCTTGTACGA CGAAGAAGCT 3670
GGCTAGCTAG CCGTCTCGAT CGTATATGTA CTGATTAAT	C TGCAGATTGA ATAAAAACTA 3730
CAGTACGCAT ATGATGCGTA CGTACGTGTG TATAGTTTG	FT GCTCATATAT GCTCCTCATC 3790
ACCTGCCTGA TCTGCCCATC GATCTCTCTC GTACTCCTT	CC CTGTTAAATG CCTTCTTTGA 3850
CAGACACACC ACCACCAGCA GCAGTGACGC TCTGCACGC	CC GCCGCTTTAA GACATGTAAG 3910
ATATTTTAAG AGGTATAAGA TACCAAGGAG CACAAATCT	TG GAGCACTGGG ATATTGCAAA 3970
GACAAAAAA AAACAAAATT AAAGTCCCAC CAAAGTAGA	AG ATAGTAAAGA GGTGGATGGA 4030
TTAAAATTAT CTCATGATTT TTGGATCTGC TCAAATAGA	AT CGATATGGTA TTCAGATCTA 4090
TGTTGTATAG CCTTTTCATT AGCTTTCTGA AAAAAAAA	rg gratgatgag tgcggagtag 4150
CTAGGGCTGT GAAGGAGTCG GATGGGCTTC CACGTACTT	rg TTTGTGGCCC TAGTCCGGTT 4210
CTATTTAGGT CCGATCCGAG TCCGGCATGG TCCGGTTCC	CA TACGGGCTAG GACCAAGCTC 4270
GGCACGTGAG TTTTAGGCCC GTCGGCTAGC CCGAGCACC	GA CCCGTTTTTA AACTGGCTAG 4330
GACTCGCCCA TTTAATAAGA CAAACATTGC AAAAAATAG	GC TCTATTTTTT ATTTAAAATA 4390
TATTGTTTAT TTGTGAAATG TGTATTATTT GTAATATAT	TA TTATTGTATA TAGTTATATC 4450
TTCAATTATG ATTTATAAAT ATGTTTTTTA TTATGAAC	TC AATTTTAAGT TTGATTTATG 4510
CGTTGGCGGG CTCGAGGAGG CACGGTGAAC ATTTTTGGC	GT CGGGCTTAAC GGGTCGGCCC 4570
GGCCCGGTTC GGCCCATCCA CGGCCCATCC CGTGTCGGC	CC TCGTTCGGTG AGTTCAGCCC 4630
GTCGGACAAC CCGTCCCCGG CCCGGATAAT TAATCGGGC	CC TAACCGTGGC GTGCTTAAAC 4690
GGTCCGTGCC TCAACGGACC GGGCCGCGG CGGCCCGT	TT GACATCTCTA GTGGTGTGAT 4750
TAGAGATGGC GATGGGAACC GATCACTGAT TCCGTGTGC	GA GAATTCGATA TCAAGCTTAT 4810
CGATACC	4817

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
- Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala
- Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser 20 25 30
- Thr Ala Thr Pro Arg Arg Tyr Asp Ala Ala Val Val Thr Thr 35 40 45
- Thr Thr Thr Ala Arg Ala Ala Ala Ala Ala Val Thr Val Pro Ala Ala 50 55 60
- Pro Pro Gln Ala Gly Arg Arg Arg Cys His Gln Ser Lys Arg Arg 65 70 75 80
- His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu 85 90 95
- Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp
- Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys
 115 120 125
- Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile
- Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly 145 150 155 160
- Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu 165 170 175
- Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser
- Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val 195 200 205
- Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 215 220
- Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu 225 230 235 240
- Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu 245 250 255
- Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg 260 265 270
- Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val 275 280 285

Ala	Val 290	Gly	Phe	Gly	Ile	Ser 295	Lys	Pro	Glu	His	Val 300	Lys	Gln	Ile	Ala	
Gln 305	Trp	Gly	Ala	Asp	Gly 310	Val	Ile	Ile	Gly	Ser 315	Ala	Met	Val	Arg	Gln 320	
Leu	Gly	Glu	Ala	Ala 325	Ser	Pro	Lys	Gln	Gly 330	Leu	Arg	Arg	Leu	Glu 335	Glu	
Tyr	Ala	Arg	Gly 340	Met	Lys	Asn	Ala	Leu 345	Pro							
(2)	INF	ORMA'	rion	FOR	SEQ	ID I	10:20):								
	(i	() () ()	QUENCA) LIB) TY	ENGTI YPE: PRANI	nuc DEDNI	349 1 leic ESS:	ase acio sino	pai:	cs							
	(ii) MO	LECUI	LE T	YPE:	CDN	A									
	(iii) HY	POTH	ETIC	AL: 1	NO										
p	olle	((n-sp osed	ATUR A) N. B) L D) O ecif in	AME/I OCAT THER ic c Figu	ION: INF alci re 3	3 ORMA um d 0."	rion epen	dent	pro	tein	kin	eque ase	nce gene	for :	maize	
TG	CAG	ልጥ ሮ	ATG Met	CAC	CAC	CTC	TCC	GGC Gly	CAG	CCC .	AAC	GTG Val	Val	GGC Gly 360	CTC Leu	47
CG(Arg	GGC GGC	GCG Ala	TAC Tyr 365	Glu	GAC Asp	AAG Lys	CAG Gln	AGC Ser 370	Val	CAC His	CTC Leu	GTC Val	ATG Met 375	Glu	CTG Leu	95
TG(Cys	C GCC s Ala	GGC Gly 380	r Gly	GAG Glu	CTC Leu	TTC Phe	GAC Asp 385	Arg	ATC	ATC Ile	GCC Ala	CGG Arg 390	СТĀ	CAG	TAC Tyr	143
AC(G GA0 C Glu 399	ı Arç	GGC GGC	GCC Ala	GCG Ala	GAG Glu 400	Leu	CTG Leu	CGC Arg	GCC Ala	ATC Ile 405	· Val	CAG Gln	ATC Ile	GTG Val	191
CAG Hi:	s Thi	TG(C CAC	TCC S Ser	ATO Met	: Gly	GTG Val	ATO Met	CAC His	CGG Arg 420	Asp	ATC	: AAG : Lys	CCC Pro	GAG Glu 425	239
AA(As:	C TTO	C CT(e Lei	G CTO	G CTC 1 Let 430	ı Ser	AAC Lys	G GAC S Asp	GAG Glu	GAC Asp 435) Ala	CCG Pro	CTO	AAC Lys	G GCC S Ala 440	C ACC Thr	287
GA:	C TT	C GG(C CTC	C TCC	C GTO	C TTC	TTC	: AAC	GAC	GGC	GAG	CTC	G CTO	C AGO	GAC	335

Asp	Phe	Gly		Ser	Val	Phe	Phe		Glu	Gly	Glu	Leu		Arg	Asp	
ATC	GTC	GGC	445 AGC	GCC	TAC	TAC	ATC	450 GCG	CCC	GAG	GTG	CTC	455 AAG	AGG	AAG	383
	Val															
	GGC Gly 475															431
	CTC Leu															479
	ACC Thr															527
	CAC His															575
	AAC Asn															623
	ATC Ile 555															671
	CTC Leu															719
	GCA Ala															767
	CTG Leu															815
	ACC Thr															863
	TCA Ser 635															911
	AAC Asn															959
	AAC Asn															1007
	GAC Asp															1055

			685					690					693			
GCC Ala	Leu	AAG Lys 700	GAG Glu	CAA Gln	GGG Gly	TTG Leu	TAT Tyr 705	GAC Asp	GCC Ala	GAT Asp	Lуs	ATC Ile 710	AAA Lys	GAC Asp	ATC Ile	1103
ATC Ile	TCC Ser 715	GAT Asp	GCC Ala	GAC Asp	TCT Ser	GAC Asp 720	AAT Asn	GAT Asp	GGA Gly	AGG Arg	ATA Ile 725	GAT Asp	TAT Tyr	TCA Ser	GAG Glu	1151
TTT Phe 730	GTG Val	GCG Ala	ATG Met	ATG Met	AGG Arg 735	AAA Lys	GGG Gly	ACG Thr	GCT Ala	GGT Gly 740	GCC Ala	GAG Glu	CCA Pro	ATG Met	AAC Asn 745	1199
ATC Ile	AAG Lys	AAG Lys	AGG Arg	CGA Arg 750	GAC Asp	ATA Ile	GTC Val	CTA Leu	TAGT	GAAG	TG A	AGCA	.GCAP	⁄G		1246
TGTG	TAAT	GT A	ATG7	GTA	ra go	CAGCI	CAA	A CAF	AGCAF	TTA	TGTA	CATO	TG T	ACAC	CAAATG	1306
CAAT	GGGG	TT A	CTTI	TGC	AA AA	AAAA	AAAZ	A AA	\AAA?	AAAA	AAA					1349
(2)	(=	ORMAT (i) S ii) A ki) S	SEQUE (A) (B) (D)	ENCE TY: TO:	CHAINGTH PE: { POLOG	RACTI : 408 amino GY: E: pi	ERIST 3 am: 5 ac: linea	rICS: ino a id ar in	acids		21:					
Gln 1	Ile	Met	His	His 5	Leu	Ser	Gly	Gln	Pro 10	Asn	Val	Val	Gly	Leu 15	Arg	
Gly	Ala	Tyr	Glu 20	Asp	Lys	Gln	Ser	Val 25	His	Leu	Val	Met	Glu 30	Leu	Cys	
Ala	Gly	Gly 35	Glu	Leu	Phe	Asp	Arg 40	Ile	Ile	Ala	Arg	Gly 45	Gln	Tyr	Thr	
Glu	Arg 50	Gly	Ala	Ala	Glu	Leu 55	Leu	Arg	Ala	Ile	Val 60	Gln	Ile	Val	His	
Thr 65	Cys	His	Ser	Met	Gly 70		Met	His	Arg	Asp 75	Ile	Lys	Pro	Glu	Asn 80	
Phe	Leu	Leu	Leu	Ser 85		Asp	Glu	Asp	Ala 90	Pro	Leu	Lys	Ala	Thr 95	Asp	
Phe	Gly	Leu	Ser 100		Phe	Phe	Lys	Glu 105	Gly	Glu	Leu	Leu	Arg 110	Asp	Ile	
Val	Gly	Ser	Ala	Tyr	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Lys 125	Arg	Lys	Tyr	

Gly Pro Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe 130 135 140

- Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe 145 150 155 160
- Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro 165 170 175
- His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile 180 185 190
- Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp 195 200 205
- Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val 210 215 220
- Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala 225 230 235 240
- Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly
 245 250 255
- Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile 260 265 270
- Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu 275 280 285
- Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly 290 295 300
- Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met 305 310 315 320
- Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe 325 330 335
- Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala 340 345 350
- Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile 355 360 365
- Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe 370 375 380
- Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile 385 390 395 400
- Lys Lys Arg Arg Asp Ile Val Leu 405
- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..464
- (D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 - Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly
 1 10 15
 - Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His 20 25 30
 - Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys 35 40 45
 - Leu Ala Ala Arg Glu Asp Val Asp Val Arg Arg Glu Val Gln Ile
 50- 55 60
 - Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala 65 70 75 80
 - Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly 85 90 95
 - Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg 100 105 110
 - Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys 115 120 125
 - His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu 130 135 140
 - Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly 145 150 155 160
 - Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly 165 170 175
 - Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro 180 185 190
 - Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala 195 200 205
 - Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala 210 215 220
 - Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile 225 230 235 240
 - Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro 245 250 255
 - Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys

260 265 270

Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp 275 280 285

Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu 290 295 300

Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Ile Thr Gly Leu Lys 305 310 315 320

Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile Thr Leu 325 330 335

Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu Ser Asp 340 345 350

Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly Asn Gly 355 360 365

Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys 370 375 380

Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys 385 390 395 400

Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys
405
410
415

Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp 420 425 430

Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe Val Ala 435 440 445

Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile Lys Lys 450 460

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..295
- (D) OTHER INFORMATION: /note= "rat protein kinase II protein sequence as shown in Figure 32."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His 55 Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly 155 Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys 200

Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu 210 215 220

Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu 225 230 235 240

Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His 245 250 255

Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln 260 265 270

Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys 275 280 285

Gly Ala Ile Leu Thr Thr Met 290 295

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..142
- (D) OTHER INFORMATION: /note= "human calmodulin protein sequence as shown in Figure 33."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe 1 5 10 15

Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met 35 40 45

Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu 50 55 60

Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu 65 70 75 80

Glu Ile Arg Glu Ala Phe Arg Val Lys Asp Lys Asp Gly Asn Gly Tyr
85 90 95

Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys

Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp 115 120 125

Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met 130 135 140

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 (B) LOCATION: 1..463

- (D) OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
 - Val Leu Pro Gln Arg Thr Gln Asn Ile Arg Glu Val Tyr Glu Val Gly
 1 5 10 15
 - Arg Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Phe Glu Cys Thr Arg 20 25 30
 - Arg Ala Ser Gly Gly Lys Phe Ala Cys Lys Ser Ile Pro Lys Arg Lys 35 40 45
 - Leu Leu Cys Lys Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile 50 55 60
 - Met His His Leu Ser Glu His Ala Asn Val Val Arg Ile Glu Gly Thr 65 70 75 80
 - Tyr Glu Asp Ser Thr Ala Val His Leu Val Met Glu Leu Cys Glu Gly
 85 90 95
 - Gly Glu Leu Phe Asp Arg Ile Val Gln Lys Gly His Tyr Ser Glu Arg
 - Gln Ala Arg Leu Ile Lys Thr Ile Val Glu Val Val Glu Ala Cys 115 120 125
 - His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu 130 135 140
 - Phe Asp Thr Ile Asp Glu Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly 145 150 155 160
 - Leu Ser Val Phe Tyr Lys Pro Gly Glu Ser Phe Cys Asp Val Val Gly 165 170 175
 - Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu Arg Lys Leu Tyr Gly Pro 180 185 190
 - Glu Ser Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser 195 200 205
 - Gly Val Pro Pro Phe Trp Ala Glu Ser Glu Pro Gly Ile Phe Arg Gln 210 215 220
 - Ile Leu Leu Gly Lys Leu Asp Phe His Ser Glu Pro Trp Pro Ser Ile 225 230 235 240
 - Ser Asp Ser Ala Lys Asp Leu Ile Arg Lys Met Leu Asp Gln Asn Pro 245 250 255
 - Lys Thr Arg Leu Thr Ala His Glu Val Leu Arg His Pro Trp Ile Val 260 265 270
 - Asp Asp Asn Ile Ala Pro Asp Lys Pro Leu Asp Ser Ala Val Leu Ser 275 280 285
 - Arg Leu Lys Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala Leu

290 295 300

Arg Val Ile Ala Glu Arg Leu Ser Glu Glu Glu Ile Gly Gly Leu Lys 305 310 315 320

- Glu Leu Phe Lys Met Île Asp Thr Asp Asn Ser Gly Thr Île Thr Phe 325 330 335
- Asp Glu Leu Lys Asp Gly Leu Lys Arg Val Gly Ser Glu Leu Met Glu 340 345 350
- Ser Glu Ile Lys Asp Leu Met Asp Ala Ala Asp Ile Asp Lys Ser Gly 355 360 365
- Thr Ile Asp Tyr Gly Glu Phe Ile Ala Ala Thr Val His Leu Asn Lys 370 375 380
- Leu Glu Arg Glu Glu Asn Leu Val Ser Ala Phe Ser Tyr Phe Asp Lys 385 390 395 400
- Asp Gly Ser Gly Tyr Ile Thr Leu Asp Glu Ile Gln Gln Ala Cys Lys 405 410 415
- Asp Phe Gly Leu Asp Asp Ile His Ile Asp Asp Met Ile Lys Glu Ile 420 425 430
- Asp Gln Asp Asn Asp Gly Gln Ile Asp Tyr Gly Glu Phe Ala Ala Met 435
- Met Arg Lys Gly Asn Gly Gly Ile Gly Arg Arg Thr Met Arg Lys 450 455 460
- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1418..1427
 - (D) OTHER INFORMATION: /note= "start of mRNA"
 - (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1481..2366
 - (ix) FEATURE:
 - (A) NAME/KEY: intron
 - (B) LOCATION: 2367..2451
 - (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 2452..2602

(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:		
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	exon 26912804	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	intron 28052906	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	exon 29073075	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	intron 30763177	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:		
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	intron 33053398	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:		
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	intron 34993713	
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	exon 37143811	
(xi)	SEQUENCE DESCR	RIPTION: SEQ ID NO:26:	
'AGTAAC	AC CTCTCCAATC G	CTTGGGTTG GCACATTCTT AGCTTTTATC ACATTTTAAG	60
ATAGAG	TT CACCACCTTC A	AAAATAATGC CTATACAATG AATGATCGCT TGGATGCAAT	120
AGCTAG	AT TCAACTAGCT A	ATATATGGTC AATAGAACCC TGTGAGCACC TCACAAACAC	180
ርጥጥር ል ል	TT TTGAGACCCT A	AGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA	240

TTA 20 AAA .80 ATA GACTTCAATT TTGAGACCCT AAGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA 240 GGACTTCTCC TTGCTAAATG CTTGTCAGCG ATCTATATAT CTTCCCCACT GCGGGAGATA 300 CTATATATAG GGCCTTGGAC CTCTAGGGTA TCTCAAAGGC CTAGTCACAA CAATTCTCAA 360 CAGTATTTAA TTTTATACAT GTATGAACAG TGTAGGAATT TGAGTGCCCA ACCCAAGAGT 420 GGGAGGTGTA AATTGGGTAG CTAAACTTAA ATAGGGCTCT TCTTATTTAG GTTTATCTAG 480 TCTCTACTTA GACTAATTCA GAAAGAATTT TACAACCTAT GGTTAATCAT ATCTCTAGTC 540

TAAGCAAATT	TAGGAAAGTT	AAAAGCACAC	AATTAGGCAC	ATGTGAAAGA	TGTGTATGGT	600
AAGTAAAAGA	CTTATAAGGA	AAAAGTGGGT	GAATCCTCAA	GATGTGGTGG	TATATCCCAA	660
TGATATTAGA	TGCCAGAATA	TAGGGGGGAA	ATCGATGTAT	ACCATCTCTA	CCAGGATACC	720
TGTGCGGACT	GTGCAACTGA	CACATGGACC	ATGGTGTCTT	CTTAGATTTG	GTTATTAGCT	780
AATTGCGCTA	CAACTTGTTC	AAGGCTAGAC	CAAATTAAAA	AACTAATATT	AAACATAAAA	840
AGTTAGGCAA	ACTATAGTAA	ATTATGCAGC	GATCCAACAA	CAAGCCATGT	CTCGTGGGTC	900
ATGAGCCACG	CGTCGGCCAT	ACACCCACAT	GATGTTTCCA	TACGGATGGT	CCTTATGCAA	960
TTTTGTCTGC	AAAACACAAG	CCTTAATACA	GCCACGCGAC	AATCATGGAA	GTGGTCGTTT	1020
TAGGTCCTCA	TCATGAAGTT	CAGGGAAAAC	GCATCAAATG	TAATGCAGAG	AAATGGTATT	1080
TCTTCTCTTG	TAAATCAGGG	AGAGGAGTAC	CATCAGTACA	GATTCAGAAT	CAGAATTCAG	1140
TCTTCCAACG	ACAATAATCG	CAGCATCTTG	TAAAAATTTG	CAGAAACTTC	TGTTTGACTT	1200
GTAGCCCTGA	- CCTTTGCAAA	TATTTGAAGT	TGTGCCTGCT	GACACAACTT	CAATCTGGAA	1260
GTGCTGTTGA	TCAGTTTTGC	CAGAAACAGC	AAGCAGCCTA	TATATATCTG	TCACGAGACA	1320
CCCTGCCGCC	CTCTTCTTTC	CCGCCATTCC	CTCCCTACCC	TTCAAAATCT	AGAAACCTTT	1380
TTTTTTCCTC	CCGATACGCC	CCTCCATCTC	TCGCCGTTCA	TGTCCGTGGC	TGGCTGCCCT	1440
CCGTGGGAGC	AGGCGGCCGC	ACTCGTTCCC	CGCCGCAGCC	ATGGGCCAGT	GCTGCTCCAA	1500
GGGCGCCGGA	GAGGCCCCGC	CACCGAGGCG	CCAAACGGCA	GGCGCCAAGC	CGCGGGCGTC	1560
CGCGAACAAC	GCCGACGGAC	AACGGGCGTC	GTCCTCGTCC	GCGGTGGCTG	CTGCCGCTGC	1620
TGCTGCCGGT	GGTGGTGGCG	GCGGCACGAC	GAAGCCGGCC	TCACCCACCG	GCGGCGCCAG	1680
GGCCAGCTCC	GGCAGCAAAC	CGGCGGCGGC	CGTGGGCACG	GTGCTGGGCC	GGCCCATGGA	1740
GGACGTGCGC	GCGACCTACT	CGATGGGCAA	GGAGCTCGGG	CGCGGGCAGT	TCGGCGTGAC	1800
GCACCTGTGC	ACGCACCGGA	CGAGCGGCGA	GAAGCTGGCG	TGCAAGACGA	TCGCGAAGCG	1860
GAAGCTGGCG	GCCAGGGAGG	ACGTGGACGA	CGTGCGGCGG	GAGGTGCAGA	TCATGCACCA	1920
CCTCTCCGGC	CAGCCCAACG	TGGTGGGCCT	CCGCGGCGCG	TACGAGGACA	AGCAGAGCGT	1980
GCACCTCGTC	ATGGAGCTGT	GCGCGGGCGG	GGAGCTCTTC	GACCGCATCA	TCGCCCGGGG	2040
CCAGTACACG	GAGCGCGGCG	CCGCGGAGCT	GCTGCGCGCC	ATCGTGCAGA	TCGTGCACAC	2100
CTGCCACTCC	: ATGGGGGTGA	TGCACCGGGA	CATCAAGCCC	GAGAACTTCC	TGCTGCTCAG	2160
CAAGGACGAG	GACGCGCCGC	TCAAGGCCAC	CGACTTCGGC	CTCTCCGTCT	TCTTCAAGGA	2220
					AGGTGCTCAA	2280
					ACATCTTCCT	

CGCCGGCGTG	CCTCCCTTCT	GGGCAGGTCG	GATCCGTCCG	TGTTCGTCCT	AGACGATATA	2400
CAGAACCCGA	CGATGGATTT	GCTTCTCAGC	CCTGTTCTTG	CATCACCAGA	GAACGAGAAC	2460
GGCATCTTCA	CCGCCATCCT	GCGAGGGCAG	CTTGACCTCT	CCAGCGAGCC	ATGGCCACAC	2520
ATCTCGCCGG	GAGCCAAGGA	TCTCGTCAAG	AAGATGCTCA	ACATCAACCC	CAAGGAGCGG	2580
CTCACGGCGT	TCCAGGTCCT	CAGTAAGTAC	CCAGATCGTT	GCTGTCATAC	ACTCATATGA	2640
ATTGTATCGT	TCATGAGCAA	CGATCGAGCG	GATTTGGTGA	ACTTGTAGAT	CACCCATGGA	2700
TCAAAGAAGA	CGGAGACGCG	CCTGACACGC	CGCTTGACAA	CGTTGTTCTC	GACAGGCTCA	2760
AGCAGTTCAG	GGCCATGAAC	CAGTTCAAGA	AAGCAGCATT	GAGGGTACAT	TATCTGATAA	2820
AAGCTCCACA	AATACAACTT	CTGAAGAACA	GCAATGCTTA	CACGGCAGAA	TTTTCATTAT	2880
AAATGCTCTT	GATGACATAA	TGTTAGATCA	TAGCTGGGTG	CCTATCCGAA	GAGGAGATCA	2940
CAGGGCTGAA	GGAGATGTTC	AAGAACATTG	ACAAGGATAA	CAGCGGGACC	ATTACCCTCG	3000
ACGAGCTCAA	ACACGGGTTG	GCAAAGCACG	GGCCCAAGCT	GTCAGACAGC	GAAATGGAGA	3060
AACTAATGGA	AGCAGTGAGT	TTTCAGAGTA	CAATCTTAAA	AAAAGGAATT	GTGATTCTTT	3120
TCAAAATGAA	GAAGTAATCT	GAAAACATCC	CTGCTGAAAT	GCTTTATACA	TTTCCAGGCT	3180
GACGCTGACG	GCAACGGGTT	AATTGACTAC	GACGAATTCG	TCACCGCAAC	AGTGCATATG	3240
AACAAACTGG	ATAGAGAAGA	GCACCTTTAC	ACAGCATTCC	AGTATTTCGA	CAAGGACAAC	3300
AGCGGGTAAG	TTGAACGTTA	AAATGATACA	GCTGGTACCT	GAATTCTGGA	CAACACATAT	3360
CATAACAGGA	CACATATATA	ATTCGTTTAT	CTCACAGGTA	CATTACTAAA	GAAGAGCTTG	3420
AGCACGCCTT	GAAGGAGCAA	GGGTTGTATG	ACGCCGATAA	AATCAAAGAC	ATCATCTCCG	3480
ATGCCGACTC	TGACAATGTA	AGGAACAAAC	ATTATTTAAA	TTTCAGCCGA	CAAACTAAAC	3540
TATAGAAACC	ACATCATGAT	ATCAAATTTT	GAGGTGGCGG	TGCTACAGAA	ATAGAACCCA	3600
GTACACCAAA	ATGACTAACT	TGTCATGATT	AGTTGTTCCT	CGTAACTGAA	CATTTGTGTT	3660
CTTAGTTTCT	TATTGTTAAA	CCAAAGACTT	AAATTCACTT	TTGCACATGC	AGGATGGAAG	3720
GATAGATTAT	TCAGAGTTTG	TGGCGATGAT	GAGGAAAGGG	ACGGCTGGTG	CCGAGCCAAT	3780
GAACATCAAG	AAGAGGCGAG	ACATAGTCCT	ATAGTGAAGT	GAAGCAGAAG	TGTGTAATGT	3840
AATGTGTATA	GCAGCTCAAA	CAAGCAAATT	TGTACATCTG	TACACAAATG	CAATGGGGTT	3900
ACTTTTGCAA	CTTAGTTCAT	GGATGGTTGT	GTACGTTGTG	CTATTGATTG	CAAGTGATTT	3960
GAAAGACATG	CATACTTAGG	AACTGAGAAA	GATAGATCTA	CTACTGCTAG	AGACAGAACA	4020
ATAGGATAAT	TCAGAAGTGG	TATTTCAGAA	GACTACAGCT	GGCATCTATT	ATTCTCATTG	4080
TCCTCGCAAA	AATACTGATG	ATGCATTTGA	GAGAACAATA	TGCAACAAGA	TCGAGCTCCC	4140
TATAGTGAGT	CGTATTAGGC	CA				4162

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)" /note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG Met	GAC Asp 410	AAC Asn	AAC Asn	CCC Pro	AAC Asn	ATC Ile 415	AAC Asn	GAG Glu	TGC Cys	ATC Ile	CCC Pro 420	TAC Tyr	AAC Asn	TGC Cys	CTG Leu	48
AGC Ser 425	AAC Asn	CCC Pro	GAG Glu	GTG Val	GAG Glu 430	GTG Val	CTG Leu	GGC Gly	GGC Gly	GAG Glu 435	CGC Arg	ATC Ile	GAG Glu	ACC Thr	GGC Gly 440	96
TAC Tyr	ACC Thr	CCC Pro	ATC Ile	GAC Asp 445	ATC Ile	AGC Ser	CTG Leu	AGC Ser	CTG Leu 450	ACC Thr	CAG Gln	TTC Phe	CTG Leu	CTG Leu 455	AGC Ser	144
GAG Glu	TTC Phe	GTG Val	CCC Pro 460	GGC Gly	GCC Ala	GGC Gly	TTC Phe	GTG Val 465	CTG Leu	GGC Gly	CTG Leu	GTG Val	GAC Asp 470	ATC Ile	ATC Ile	192
TGG Trp	GGC Gly	ATC Ile 475	TTC Phe	GGC Gly	CCC Pro	AGC Ser	CAG Gln 480	TGG Trp	GAC Asp	GCC Ala	TTC Phe	CTG Leu 485	GTG Val	CAG Gln	ATC Ile	240
GAG Glu	CAG Gln 490	CTG Leu	ATC Ile	AAC Asn	CAG Gln	CGC Arg 495	ATC Ile	GAG Glu	GAG Glu	TTC Phe	GCC Ala 500	CGC Arg	AAC Asn	CAG Gln	GCC Ala	288
ATC Ile 505	AGC Ser	CGC Arg	CTG Leu	GAG Glu	GGC Gly 510	CTG Leu	AGC Ser	AAC Asn	CTG Leu	TAC Tyr 515	CAA Gln	ATC Ile	TAC Tyr	GCC Ala	GAG Glu 520	336
AGC Ser	TTC Phe	CGC Arg	GAG Glu	TGG Trp 525	GAG Glu	GCC Ala	GAC Asp	CCC Pro	ACC Thr 530	AAC Asn	CCC Pro	GCC Ala	CTG Leu	CGC Arg 535	GAG Glu	384
GAG Glu	ATG Met	CGC Arg	ATC Ile 540	CAG Gln	TTC Phe	AAC Asn	GAC Asp	ATG Met 545	AAC Asn	AGC Ser	GCC Ala	CTG Leu	ACC Thr 550	ACC Thr	GCC Ala	432

ATC Ile	CCC Pro	CTG Leu 555	TTC Phe	GCC Ala	GTG Val	CAG Gln	AAC Asn 560	TAC Tyr	CAG Gln	GTG Val	CCC Pro	CTG Leu 565	CTG Leu	AGC Ser	GTG Val	48	30
TAC Tyr	GTG Val 570	CAG Gln	GCC Ala	GCC Ala	AAC Asn	CTG Leu 575	CAC His	CTG Leu	AGC Ser	GTG Val	CTG Leu 580	CGC Arg	GAC Asp	GTC Val	AGC Ser	52	28
GTG Val 585	TTC Phe	GGC Gly	CAG Gln	CGC Arg	TGG Trp 590	GGC Gly	TTC Phe	GAC Asp	GCC Ala	GCC Ala 595	ACC Thr	ATC Ile	AAC Asn	AGC Ser	CGC Arg 600	57	76
TAC Tyr	AAC Asn	GAC Asp	CTG Leu	ACC Thr 605	CGC Arg	CTG Leu	ATC Ile	GGC Gly	AAC Asn 610	TAC Tyr	ACC Thr	GAC Asp	CAC His	GCC Ala 615	GTG Val	62	24
CGC Arg	TGG Trp	TAC Tyr	AAC Asn 620	ACC Thr	GGC Gly	CTG Leu	GAG Glu	CGC Arg 625	GTG Val	TGG Trp	GGT Gly	CCC Pro	GAC Asp 630	AGC Ser	CGC Arg	67	72
GAC Asp	TGG Trp	ATC Ile 635	AGG Arg	TAC Tyr	AAC Asn	CAG Gln	TTC Phe 640	CGC Arg	CGC Arg	GAG Glu	CTG Leu	ACC Thr 645	CTG Leu	ACC Thr	GTG Val	72	20
CTG Leu	GAC Asp 650	ATC Ile	GTG Val	AGC Ser	CTG Leu	TTC Phe 655	CCC Pro	AAC Asn	TAC Tyr	GAC Asp	AGC Ser 660	CGC Arg	ACC Thr	TAC Tyr	CCC Pro	76	68
ATC Ile 665	CGC Arg	ACC Thr	GTG Val	AGC Ser	CAG Gln 670	CTG Leu	ACC Thr	CGC Arg	GAG Glu	ATT Ile 675	TAC Tyr	ACC Thr	AAC Asn	CCC Pro	GTG Val 680	81	16
CTG Leu	GAG Glu	AAC Asn	TTC Phe	GAC Asp 685	GGC Gly	AGC Ser	TTC Phe	CGC Arg	GGC Gly 690	AGC Ser	GCC Ala	CAG Gln	GGC Gly	ATC Ile 695	GAG Glu	8	64
GGC Gly	AGC Ser	ATC Ile	CGC Arg 700	AGC Ser	CCC Pro	CAC His	CTG Leu	ATG Met 705	Asp	ATC Ile	CTG Leu	AAC Asn	AGC Ser 710	ATC Ile	ACC Thr	9:	12
ATC Ile	TAC Tyr	ACC Thr 715	Asp	GCC Ala	CAC His	CGC Arg	GGC Gly 720	Glu	TAC Tyr	TAC Tyr	TGG Trp	AGC Ser 725	GGC Gly	CAC His	CAG Gln	9	60
ATC Ile	ATG Met 730	Ala	AGC Ser	CCC Pro	GTC Val	GGC Gly 735	TTC Phe	AGC Ser	GGC Gly	CCC Pro	GAG Glu 740	Pne	ACC Thr	TTC Phe	CCC Pro	10	80
CTG Leu 745	Tyr	GGC Gly	ACC Thr	ATG Met	GGC Gly 750	Asn	GCT Ala	GCA Ala	CCT Pro	CAG Gln 755	Gln	CGC Arg	ATC Ile	GTG Val	GCA Ala 760	10	56
CAG Gln	CTG Leu	GGC Gly	CAG Gln	GGA Gly 765	Val	TAC Tyr	CGC Arg	ACC Thr	CTG Leu 770	AGC Ser	AGC Ser	ACC Thr	CTG Leu	TAC Tyr 775	CGT Arg	11	.04
CGA Arg	CCT Pro	TTC Phe	AAC Asn 780	. Ile	GGC Gly	ATC Ile	AAC Asn	AAC Asn 785	Gln	CAG Gln	CTG Leu	AGC Ser	GTG Val 790	Leu	GAC Asp	11	.52

GGC Gly	ACC Thr	GAG Glu 795	TTC Phe	GCC Ala	TAC Tyr	GGC Gly	ACC Thr 800	AGC Ser	AGC Ser	AAC Asn	CTG Leu	CCC Pro 805	AGC Ser	GCC Ala	GTG Val	1200
TAC Tyr	CGC Arg 810	AAG Lys	AGC Ser	GGC Gly	ACC Thr	GTG Val 815	GAC Asp	AGC Ser	CTG Leu	GAC Asp	GAG Glu 820	ATC Ile	CCC Pro	CCT Pro	CAG Gln	1248
AAC Asn 825	AAC Asn	AAC Asn	GTG Val	CCA Pro	CCT Pro 830	CGA Arg	CAG Gln	GGC Gly	TTC Phe	AGC Ser 835	CAC His	CGT Arg	CTG Leu	AGC Ser	CAC His 840	1296
GTG Val	AGC Ser	ATG Met	TTC Phe	CGC Arg 845	AGT Ser	GGC Gly	TTC Phe	AGC Ser	AAC Asn 850	AGC Ser	AGC Ser	GTG Val	AGC Ser	ATC Ile 855	ATC Ile	1344
CGT Arg	GCA Ala	CCT Pro	ATG Met 860	TTC Phe	AGC Ser	TGG Trp	ATT Ile	CAC His 865	CGC Arg	AGT Ser	GCC Ala	GAG Glu	TTC Phe 870	AAC Asn	AAC Asn	1392
ATC Ile	ATC Ile	CCC Pro 875	Ser	AGC Ser	CAG Gln	ATC Ile	ACC Thr 880	CAG Gln	ATC Ile	CCC Pro	CTG Leu	ACC Thr 885	AAG Lys	AGC Ser	ACC Thr	1440
Asn	Leu 890	Gly	Ser	Gly	Thr	Ser 895	Val	Val	AAG Lys	Gly	900	Gly	Phe	Thr	GIA	1488
GGC Gly 905	GAC Asp	ATC Ile	CTG Leu	CGC Arg	CGC Arg 910	ACC Thr	AGC Ser	CCC Pro	GGC Gly	CAG Gln 915	ATC Ile	AGC Ser	ACC Thr	CTG Leu	CGC Arg 920	1536
GTG Val	AAC Asn	ATC Ile	ACC Thr	GCC Ala 925	CCC Pro	CTG Leu	AGC Ser	CAG Gln	CGC Arg 930	TAC Tyr	CGC Arg	GTC Val	CGC Arg	ATC Ile 935	CGC Arg	1584
TAC Tyr	GCC Ala	AGC Ser	ACC Thr 940	ACC Thr	AAC Asn	CTG Leu	CAG Gln	TTC Phe 945	CAC His	ACC Thr	AGC Ser	ATC Ile	GAC Asp 950	GGC Gly	CGC Arg	1632
CCC Pro	ATC Ile	AAC Asn 955	CAG Gln	GGC Gly	AAC Asn	TTC Phe	AGC Ser 960	GCC Ala	ACC Thr	ATG Met	AGC Ser	AGC Ser 965	GGC Gly	AGC Ser	AAC Asn	1680
CTG Leu	CAG Gln 970	AGC Ser	GGC Gly	AGC Ser	TTC Phe	CGC Arg 975	ACC Thr	GTG Val	GGC Gly	TTC Phe	ACC Thr 980	ACC Thr	CCC Pro	TTC Phe	AAC Asn	1728
TTC Phe 985	AGC Ser	AAC Asn	GGC Gly	AGC Ser	AGC Ser 990	GTG Val	TTC Phe	ACC Thr	CTG Leu	AGC Ser 995	GCC Ala	CAC His	GTG Val	TTC Phe	AAC Asn 1000	1776
AGC Ser	GGC Gly	AAC Asn	GAG Glu	GTG Val 100	Tyr	ATC Ile	GAC Asp	CGC Arg	ATC Ile 101	Glu	TTC Phe	GTG Val	CCC Pro	GCC Ala 101	Glu	1824
GTG Val	ACC Thr	TTC Phe	GAG Glu 102	Ala	GAG Glu	TAC Tyr	GAC Asp	CTG Leu 102	GAG Glu 5	AGG Arg	GCT Ala	CAG Gln	AAG Lys 103	Ala	GTG Val	1872
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920

Asn Glu Leu Phe 1035	Thr Ser Ser Ass		Leu Lys Thr Asp 1045	Val
ACC GAC TAC CAC Thr Asp Tyr His 1050	ATC GAT CAA GT Ile Asp Gln Va 1055	A TCC AAT TTA L Ser Asn Leu	GTT GAG TGT TTA Val Glu Cys Leu 1060	TCT 1968 Ser
GAT GAA TTT TGT Asp Glu Phe Cys 1065	CTG GAT GAA AA Leu Asp Glu Ly 1070	A AAA GAA TTG s Lys Glu Leu 1079	TCC GAG AAA GTC Ser Glu Lys Val 5	AAA 2016 Lys 1080
CAT GCG AAG CGA His Ala Lys Arg	CTT AGT GAT GA Leu Ser Asp Gl 1085	G CGG AAT TTA 1 Arg Asn Leu 1090	CTT CAA GAT CCA Leu Gln Asp Pro 109	Asn
TTT AGA GGG ATO Phe Arg Gly Ile 110	Asn Arg Gln Le	A GAC CGT GGC 1 Asp Arg Gly 1105	TGG AGA GGA AGT Trp Arg Gly Ser 1110	ACG 2112 Thr
GAT ATT ACC ATC Asp Ile Thr Ile 1115	CAA GGA GGC GA Gln Gly Gly As 11	p Asp Val Phe	AAA GAG AAT TAC Lys Glu Asn Tyr 1125	GTT 2160 Val
ACG CTA TTG GGT Thr Leu Leu Gly 1130	ACC TTT GAT GA Thr Phe Asp Gl 1135	G TGC TAT CCA u Cys Tyr Pro	ACG TAT TTA TAT Thr Tyr Leu Tyr 1140	CAA 2208 Gln
AAA ATA GAT GAG Lys Ile Asp Glu 1145	TCG AAA TTA AA Ser Lys Leu Ly 1150	A GCC TAT ACC s Ala Tyr Thr 115	CGT TAC CAA TTA Arg Tyr Gln Leu 5	AGA 2256 Arg 1160
GGG TAT ATC GAR Gly Tyr Ile Glu	A GAT AGT CAA GA A Asp Ser Gln As 1165	C TTA GAA ATC p Leu Glu Ile 1170	TAT TTA ATT CGC Tyr Leu Ile Arg 117	Tyr
AAT GCC AAA CAC Asn Ala Lys His	s Glu Thr Val As	T GTG CCA GGT n Val Pro Gly 1185	ACG GGT TCC TTA Thr Gly Ser Leu 1190	TGG 2352 Trp
CCG CTT TCA GCC Pro Leu Ser Ala 1195	a Pro Ser Pro Il	e Gly Lys Cys	GGG GAG CCG AAT Gly Glu Pro Asr 1205	CGA 2400 Arg
TGC GCT CCG CAC Cys Ala Pro His 1210	C CTG GAG TGG AA S Leu Glu Trp As 1215	C CCG GAC CTA n Pro Asp Leu	GAC TGC AGC TGC Asp Cys Ser Cys 1220	AGG 2448 Arg
GAC GGG GAG AAG Asp Gly Glu Ly: 1225	G TGC GCC CAT CA S Cys Ala His Hi 1230	T TCC CAT CAT s Ser His His 123	TTC TCC TTG GAC Phe Ser Leu Asy 5	C ATT 2496 O Ile 1240
GAT GTT GGA TG Asp Val Gly Cy	r ACA GAC TTA AA s Thr Asp Leu As 1245	T GAG GAC TTA n Glu Asp Leu 1250	GGT GTA TGG GTG Gly Val Trp Val 129	rire
TTC AAG ATT AAG Phe Lys Ile Lys 12	s Thr Gln Asp Gl	C CAT GCA AGA y His Ala Arg 1265	CTA GGA AAT CTA Leu Gly Asn Leu 1270	A GAA 2592 1 Glu
TTT CTC GAA GA	G AAA CCA TTA GT 1 Lys Pro Leu Va	'A GGA GAA GCA	CTA GCT CGT GTG Leu Ala Arg Va	G AAA 2640 L Lys

1275 1280 1285

AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 1290 1295 1300	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 1305 1310 1315 1320	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 1325 1330 1335	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 1340 1345 1350	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 1355 1360 1365	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 1370 1375 1380	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 1385 1390 1395 1400	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 1405 1410 1415	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1420 1425 1430	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1435 1440 1445	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1450 1460	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1465 1470 1475 1480	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1485 1490 1495	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1500 1505 1510	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1515 1520 1525	3360

GAT Asp	GGA Gly 1530	Arg	AGA Arg	GAC Asp	Asn	CCT Pro 1535	Cys	GAA Glu	TCT Ser	AAC Asn	AGA Arg 1540	Gly	TAT Tyr	GGG Gly	GAT Asp	3408
TAC Tyr 1545	Thr	CCA Pro	CTA Leu	CCA Pro	GCT Ala 1550	Gly	TAT Tyr	GTG Val	ACA Thr	AAA Lys 1555	Glu	TTA Leu	GAG Glu	TAC Tyr	TTC Phe 1560	3456
CCA Pro	GAA Glu	ACC Thr	GAT Asp	AAG Lys 1565	Val	TGG Trp	ATT Ile	GAG Glu	ATC Ile 1570	GGA Gly)	GAA Glu	ACG Thr	GAA Glu	GGA Gly 1575	Thr	3504
				Ser					Leu	ATG Met			TAA			3546

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1181 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175

- Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190
- Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205
- Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220
- Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240
- Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
- Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270
- Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285
- Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300
- Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315 320
- Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335
- Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350
- Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
- Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380
- Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400
- Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415
- Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430
- Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 435 440 445
- Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 450 455 460
- Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 465 470 475 480
- Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 505 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 520 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 570 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 615 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 630 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 650 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 660 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 680 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 695 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 725 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 745 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 755 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 780 775 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 790 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 810

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile

820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 855

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165	
Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180	
(2) INFORMATION FOR SEQ ID NO:29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 88 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE74A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GCAGATCTGG ATCCATGCAC GCCGTGAAGG GCCCTTCTAG AAGGCCTATC GATAAAGAGC	60
TCCCCGGGGA TGGATTGCAC GCAGGTTC	88
(2) INFORMATION FOR SEQ ID NO:30:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE72A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GCGTTAACAT GTCGACTCAG AAGAACTCGT CAAGAAGGCG	40
(2) INFORMATION FOR SEQ ID NO:31:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P1(a)"</pre>	
(iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GTCGACAAGG ATCCAACAAT GG	22
(2) INFORMATION FOR SEQ ID NO:32:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P1(b)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
AATTGTCGAC AAGGATCCAA CAATGG	26
(2) INFORMATION FOR SEQ ID NO:33:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P2(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
ACACGCTGAC GTCGCGCAGC ACG	23
(2) INFORMATION FOR SEQ ID NO:34:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P2(b)"</pre>	
(iii) HYDOTHETICAL, NO	

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AGCTACACG	C TGACGTCGCG CAG	23
(2) INFOR	MATION FOR SEQ ID NO:35:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer A1"	
(iii)	HYPOTHETICAL: NO	
(====)		
	SEQUENCE DESCRIPTION: SEQ ID NO:35:	
AATTGTCGA		10
(2) INFOR	MATION FOR SEQ ID NO:36:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer A2"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:36:	
GCGTGTAGC	т	10
(2) INFOR	MATION FOR SEQ ID NO:37:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) 1	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P3(a)"	
(iii) 1	HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GCTGCGCGAC GTCAGCGTGT TCGG	24
(2) INFORMATION FOR SEQ ID NO:38:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P3(b)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
AATTGCTGCG CGACGTCAGC GTG	23
(2) INFORMATION FOR SEQ ID NO:39:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P4(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GGCGTTGCCC ATGGTGCCGT ACAGG	25
(2) INFORMATION FOR SEQ ID NO:40:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P4(b)"</pre>	
(iii) HYPOTHETICAL: NO	

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:40:	
AGCTGGCG	TT GCCCATGGTG CCG	23
(2) INFO	RMATION FOR SEQ ID NO:41:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer B1"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:41:	
AATTGCTG	CG	10
(2) INFOR	RMATION FOR SEQ ID NO:42:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer B2"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
AACGCCAGC	•	10
	RMATION FOR SEQ ID NO:43:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P5(a)"	
(iii)	HYPOTHETICAL: NO	

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43:	
TTCCCCCT	GT ACGGCACCAT GGGCAACGCC GC	32
(2) INFO	RMATION FOR SEQ ID NO:44:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P5(b)"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
AATTGTAC	GG CACCATGGGC AAC	23
(2) INFO	RMATION FOR SEQ ID NO:45:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P6(a)"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:45:	
GAAGCCGG	GG CCCTTCACCA CGCTGG	26
(2) INFO	RMATION FOR SEQ ID NO:46:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P6(b)"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:46:	

AGCTGAAGCC GGGGCCCTTC ACC	23
(2) INFORMATION FOR SEQ ID NO:47:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer C1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
AATTGTACGG	10
(2) INFORMATION FOR SEQ ID NO:48:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer C2 - first half"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
TTCCCCTGTA CGG	13
(2) INFORMATION FOR SEQ ID NO:49:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: other nucleic acid	

- - (A) DESCRIPTION: /desc = "primer C1 second half
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCTTCAG	CT	10
(2) INFO	RMATION FOR SEQ ID NO:50:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer PEPCivs#9 - forward"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:50:	
GTACAAAA	AC CAGCAACTC	19
(2) INFO	RMATION FOR SEQ ID NO:51:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer PEPCivs#9 reverse"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:51:	
CTGCACAA	AG TGGAGTAGT	19
(2) INFOR	RMATION FOR SEQ ID NO:52:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P7(a)"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:52:	
TGGTGAAGG	G CCCCGGCTTC ACCGG	25

(2) INFO	RMATION FOR SEQ ID NO:53:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P8(a)"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:53:	
ATCATCGAT	IG AGCTCCTACA CCTGATCGAT GTGGTA	36
(2) INFO	RMATION FOR SEQ ID NO:54:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) second	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer for fourth quarter - half"	
(iii)	HYPOTHETICAL: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO:54:	20
(2) INFOR	RMATION FOR SEQ ID NO:55:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) first h	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer for third quarter - nalf"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEO ID NO:55:	

TTCCCCCTGT A	11
(2) INFORMATION FOR SEQ ID NO:56:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer MK23A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
GGGGCTGCGG ATGCTGCCCT	20
	20
(2) INFORMATION FOR SEQ ID NO:57:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer MK25A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
GAGCTGACCC TGACCGTGCT	20
(2) INFORMATION FOR SEQ ID NO:58:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer MK26A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
CACCTGATGG ACATCCTGAA	20

(2) INFOR	RMATION FOR SEQ ID NO:59:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) to dele	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "sequence in pCIB3073 prior etion"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:59:	
TATAAGGAT	TC CCGGGGGCAA GATCTGAGAT ATG	33
(2) TNFO	RMATION FOR SEQ ID NO:60:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE134A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:60:	
CGTGACCG	AC TACCACATCG ATCAAGTATC CAATTTAGTT GAGT	44
(2) INFO	RMATION FOR SEQ ID NO:61:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE135A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:61:	
ACTCAACT	AA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG	44

(2) INFORMATION FOR SEQ ID NO:62:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE136A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT	37
(2) INFORMATION FOR SEQ ID NO:63:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE137A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GCTGATTATG CATCAGCCTA T	21
(2) INFORMATION FOR SEQ ID NO:64:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE138A28"</pre>	
(iii) HYPOTHETICAL: NO	

38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTC

(2) INFO	RMATION FOR SEQ ID NO:65:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer MK05A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:65:	
CAAAGGTA	CC CAATAGCGTA ACG	23
(2) INFO	RMATION FOR SEQ ID NO:66:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer MK35A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:66:	
AACGAGGT	GT ACATCGACCG	20
(2) INFO	RMATION FOR SEQ ID NO:67:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "forward primer for	
pCIB443	34"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:67:	
GCACCGATA	AT CACCATCCAA GGAGGCGATG ACGTATTCAA AG	42

(2) INFORMATION FOR SEQ ID NO:68:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "reverse primer for pCIB4434"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
AGCGCATCGA TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G	51
(2) INFORMATION FOR SEQ ID NO:69:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	30
ATTACGTTAC GCTATTGGGT ACCTTTGATG	30
(2) INFORMATION FOR SEQ ID NO:70:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #2"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA	60

(iii) HYPOTHETICAL: NO

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(2) INFORMATION FOR SEQ ID NO:71:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #3"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
CAAGTGCGGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGGAACCCGG ACCTAGACTG	60
CAGCTGCAGG GACGGGGAAA AATGTGCCCA TCATTCCC	98
(2) INFORMATION FOR SEQ ID NO:72:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #4"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
TGGTTTCTCT TCGAGAAATT CTAGATTTCC	30
(2) INFORMATION FOR SEQ ID NO:73:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer used to map transcriptional start site for TrpA gene"</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCGTTCGTTC CTCCTTCGTC GAGG

24

- (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..26
 - (D) OTHER INFORMATION: /note= "N-terminal peptide from pollen specific protein"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Thr Pro Leu Thr Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His
1 5 10 15

Leu Ile Leu Thr Pro Asn Val Ala Thr Ile 20 25

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /note= "internal peptide of pollen specific protein"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Val Val Ile Lys 20

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Gly Gly Thr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe Lys 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..12
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu His Gly Gly Asp Asp Phe Ser Phe Thr Leu Lys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Glu Gly Pro Thr Gly Thr Trp Thr Leu Asp Thr Lys

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide #51"
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AARTCRTCAB CACCRTGYTC

20

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide #58"
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCC	CA CYTGRAA	1 7
(2) INFO	RMATION FOR SEQ ID NO:81:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide PE51"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:81:	
TGGCCCAT	GG CTGCGGCGGG GAACGAGTGC GGC	33
(2) INFO	RMATION FOR SEQ ID NO:82:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #42"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:82:	
AGCGGTCG	AC CTGCAGGCAT GCGATCTGCA CCTCCCGCCG	40
(2) INFO	RMATION FOR SEQ ID NO:83:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #43"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:	

ATGGGCAA	GG AGCTCGGG	18
(2) INFO	RMATION FOR SEQ ID NO:84:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #SK50"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CCCTTCAA	AA TCTAGAAACC T	21
(2) INFO	RMATION FOR SEQ ID NO:85:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer #SK49"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TAATGTCG	AC GAACGGCGAG AGATGGA	27
(2) INFO	RMATION FOR SEQ ID NO:86:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE99A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:86:	
TGCGGTTA	CC GCCGATCACA TG	22

(2) INF	ORMATION FOR SEQ ID NO:87:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE97A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:87:	
	CGC GTCGACGCGG ATCCCGCGGC GGGAAGCTAA G	41
(2) INFO	DRMATION FOR SEQ ID NO:88:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE100A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:88:	
	CC GCAACA	1.0
		16
	RMATION FOR SEQ ID NO:89:	
(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE98A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:89:	
1224	SANGE SECULATION. SEX IN MO.O.:	

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC

(2) INFORMATION FOR SEQ ID NO:90:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE104A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
GATGTCGTCG ACCGCAACAC	20
(2) INFORMATION FOR SEQ ID NO:91:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE103A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
GCGGTACCGC GGATCCTGTC CGACACCGGA CGGCT	35
(2) INFORMATION FOR SEQ ID NO:92:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE127"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
GCGGATCCGG CTGCGGCGGG GAACGA	26
(2) INFORMATION FOR SEQ ID NO:93:	

(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE150A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:93:	
ATTCGCAT	GC ATGTTTCATT ATC	23
(2) INFO	RMATION FOR SEQ ID NO:94:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer KE151A28"	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:94:	
	CA CGGATCCGTC GCTTCTGTGC AACAACC	37
GCIGGIAC	COUNTECOTO OCTICIONO INMINIO	